



CC also be used to treat conditions exacerbated by the activities of Th-1  
 CC type cytokines, or Listeria. Toxoplasma or Mycobacterium infection. Its  
 CC ability to selectively or partially block the LT-beta-R pathway may be  
 CC useful in the treatment of abnormal lymphoid organ development associated  
 CC with misexpression or overexpression of signalling by the LT-beta-R.  
 CC The present LT-beta R blocking agent is capable of selectively  
 CC inhibiting this, but not the T cell dependent effector mechanisms. As  
 CC Th1 cytokines can inhibit Th2 cell dependent responses, the present LT-  
 CC beta-R blocking agent may also indirectly stimulate certain Th2 cell  
 CC dependent responses which are normally inhibited by the induced  
 CC cytokines. Doses of about 1 mg/kg of the present soluble LT-beta-R are  
 CC expected to be suitable starting doses for optimising treatment

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SQ Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 1.2e-78; Mismatches 0; Indels 0; Gaps 0;

Db 1 SQPQAVPPYASENOTCRDQEKEYEPORHICCSRCPPGTYSAKCSRIRDTCATCAENS 60

Db 1 SQPQAVPPYASENOTCRDQEKEYEPORHICCSRCPPGTYSAKCSRIRDTCATCAENS 60

Qy 61 YNEHHWNYLTICOLCRPCDPVMLEIAPCTSKRTQCRTOCQPMFCAAWALECTCELLSD 120

Db 61 YNEHHWNYLTICOLCRPCDPVMLEIAPCTSKRTQCRTOCQPMFCAAWALECTCELLSD 120

Qy 121 CPPGTEAKLDEVKGNHNHCVPCKAGHIFTONTSSPSARCOPIHTRCENQGLVEAAPGTAQSD 180

Db 121 CPPGTEAKLDEVKGNHNHCVPCKAGHIFTONTSSPSARCOPIHTRCENQGLVEAAPGTAQSD 180

Qy 181 TTCKNPLPLEPLPPPEMSGT 197

Db 181 TTCKNPLPLEPLPPPEMSGT 197

Qy 181 TTCKNPLPLEPLPPPEMSGT 197

Db 181 TTCKNPLPLEPLPPPEMSGT 197

## RESULT 2

ID AAY31326 Standard; peptide; 197 AA.

XX

AC AAY31326;

XX

DT 04-OCT-1999 (first entry)

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DE Human lymphotoxin (LT) beta-receptor extracellular region.

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KW Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell;

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KW immune system; tumour; follicular lymphoma; extracellular domain; human.

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OS Homo sapiens.

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PN WO9938525-A1.

XX

PD 05-AUG-1999.

XX

PR 29-JAN-1999; 99WO-US001928.

XX

PR 30-JAN-1998; 98US-0073112P.

XX

PR 02-FEB-1998; 98US-0073410P.

XX

PA (BIOJ ) BIOGEN INC.

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PI Browning J, Thorbecke J, Tsaiagbe V;

XX

DR WPI; 1999-4-65242/39.

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PT New method of treating follicular lymphomas by inhibiting interaction

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PT between lymphotoxin-beta and its receptor.

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PS Example 1; Page 25-26; 31pp; English.

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CC The invention provides a method for arresting or reducing, severity of

CC effects of a tumour by administration of a composition which inhibits the

CC interaction between lymphotoxin (LT)-beta and its receptor. An inhibitor  
 CC of the interaction between LT-beta and its receptor can be administered  
 CC for altering the survival or maintenance of follicular dendritic cells in  
 CC a subject and for altering the architecture of the organs of the immune  
 CC system. The method is useful for treating tumours, specifically  
 CC follicular lymphomas. It offers an alternative therapy for those with  
 CC tumours resistant to traditional chemotherapy. The present sequence  
 CC represents the extracellular region of the human LTbeta receptor and  
 CC comprises the ligand binding domain

XX

SQ Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 1.2e-78; Mismatches 0; Indels 0; Gaps 0;

Db 1 SQPQAVPPYASENOTCRDQEKEYEPORHICCSRCPPGTYSAKCSRIRDTCATCAENS 60

Db 1 SQPQAVPPYASENOTCRDQEKEYEPORHICCSRCPPGTYSAKCSRIRDTCATCAENS 60

Qy 61 YNEHHWNYLTICOLCRPCDPVMLEIAPCTSKRTQCRTOCQPMFCAAWALECTCELLSD 120

Db 61 YNEHHWNYLTICOLCRPCDPVMLEIAPCTSKRTQCRTOCQPMFCAAWALECTCELLSD 120

Qy 121 CPPGTEAKLDEVKGNHNHCVPCKAGHIFTONTSSPSARCOPIHTRCENQGLVEAAPGTAQSD 180

Db 121 CPPGTEAKLDEVKGNHNHCVPCKAGHIFTONTSSPSARCOPIHTRCENQGLVEAAPGTAQSD 180

Qy 181 TTCKNPLPLEPLPPPEMSGT 197

Db 181 TTCKNPLPLEPLPPPEMSGT 197

Qy 181 TTCKNPLPLEPLPPPEMSGT 197

Db 181 TTCKNPLPLEPLPPPEMSGT 197

RESULT 3  
ADO43009  
ID ADO43009 standard; protein; 197 AA.

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AC ADO43009;

XX

DT 29-JUL-2004 (first entry)

XX

DE Lymphotoxin-beta receptor (soluble form).

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XX Human Lymphotoxin-beta receptor; receptor; immunomodulator; anti-rheumatic; antiarthritic; antidiabetic; urologic; dermatological.

XX

OS Homo sapiens.

XX

EN WO2004039329-A2.

XX

PD 13-MAY-2004.

XX

PP 31-OCT-2003; 2003WO-US034813.

XX

PR 31-OCT-2002; 2002US-0422588P.

XX

(BIOJ ) BIOGEN INC.

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PT Treating an animal having an immunological renal disorder or glomerulonephritis comprising administering to the mammal a composition comprising an inhibitor of the lymphotoxin (LT) pathway.

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PI Comerman J, Browning JL;

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DR WPI; 2004-376051/35.

XX

CC The present is the protein sequence of a soluble lymphotoxin-beta receptor (LTBR) comprising the extracellular domain of LTBR that is CC capable of binding lymphotoxin (LT) specifically. The invention provides CC methods for treating immunological disorders, including pathologies CC associated with immunoglobulin deposits in the kidneys. It is based in

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part on the discovery that inhibition of the LT pathway with a soluble form of LTBR leads to amelioration of lupus-like disease in BAFF-transgenic mice. It is also based in part on the discovery that renal dysfunction in BAFF-transgenic mice is associated with accumulation of IgA and IgM immune complexes in the kidneys. Methods are provided for treating immunological diseases, including diseases caused by dysregulated production of immunoglobulins by B cells including dysregulated production of IgA or IgG. Compositions comprising inhibitors of the LT pathway are used to prevent or treat pathologies associated with renal dysfunction accompanied by immunoglobulin deposits, including glomerulonephritis. Suitable inhibitors include soluble forms of LTBR. The methods are useful for treating an immunological renal disorder, e.g. systemic lupus erythematosus, Sjogren's syndrome, rheumatoid arthritis, insulin-dependent diabetes mellitus, chronic hepatitis, Henoch-Schonlein purpura, IgA nephropathy or glomerulonephritis.

The invention relates to novel ovarian specific nucleic acid molecules and the polypeptides encoded by them. A protein of the invention has cyrostatic and immunostimulant activity. A nucleic acid of the invention may have as a vaccine, and in gene therapy. The nucleic acid molecule or polypeptide, antibody or peptide is useful in identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non cancerous disease states in ovarian tissue and inducing an immune response against the ovarian cancer cell. The sequences shown in AD067535-AD67682 represent ovarian specific polypeptides of the invention.

Sequence 197 AA;			
Query	Match	Score	Length
SQ		100.0% ; Best Local Similarity Matches 197; Conservative	1133; DB 8; Pred. No. 1, 2e-78; 0; Mismatches 0;
Qy		1 SQPQAVPPYASENOTCRDQEKEYYEQHRIICSSRCPGTYVSACKSR1RTDVCAENS 1 SQPQAVPPYASENOTCRDQEKEYYEQHRIICSSRCPGTYVSACKSR1RTDVCAENS	Length 197;
Db		1 YNEHHWNLTLICOLCRPCDPVNGLEBIAPTSKRKTQCRCPGMFCAAWALECTCELLSD 1 YNEHHWNLTLICOLCRPCDPVNGLEBIAPTSKRKTQCRCPGMFCAAWALECTCELLSD	60
Qy		61 YNEHHWNLTLICOLCRPCDPVNGLEBIAPTSKRKTQCRCPGMFCAAWALECTCELLSD 61 YNEHHWNLTLICOLCRPCDPVNGLEBIAPTSKRKTQCRCPGMFCAAWALECTCELLSD	60
Db		61 CPPGTEAELKDEVGKNNHCVPKACHFQNTSSPSARCPHTRCENGVLVEAPGTAQSD 61 CPPGTEAELKDEVGKNNHCVPKACHFQNTSSPSARCPHTRCENGVLVEAPGTAQSD	120
Qy		61 CPPGTEAELKDEVGKNNHCVPKACHFQNTSSPSARCPHTRCENGVLVEAPGTAQSD 61 CPPGTEAELKDEVGKNNHCVPKACHFQNTSSPSARCPHTRCENGVLVEAPGTAQSD	120
Db		120 CPPGTEAELKDEVGKNNHCVPKACHFQNTSSPSARCPHTRCENGVLVEAPGTAQSD 120 CPPGTEAELKDEVGKNNHCVPKACHFQNTSSPSARCPHTRCENGVLVEAPGTAQSD	180
Qy		121 CPPGTEAELKDEVGKNNHCVPKACHFQNTSSPSARCPHTRCENGVLVEAPGTAQSD 121 CPPGTEAELKDEVGKNNHCVPKACHFQNTSSPSARCPHTRCENGVLVEAPGTAQSD	180
Db		121 TTKRNPLPLPEMSGT 197 121 TTKRNPLPLPEMSGT 224	207

RESULT 5  
ABP96137  
TTCKNPBLELPPPEMSGT 1.97  
TTCKNPBLELPPPEMSGT 1.97

ABP9613 / Standard; protein; 433 AA.  
XX  
AC ABP96137;  
PRESSURE T 4

ADJ67643 standard protein; 305 AA.  
XX DT 09-MAY-2003 (first entry)

XX DE Human TNF receptor 2 related protein/LtRbeta SEQ ID NO:19.  
XX DE ADJ67643;  
XX DE

06-MAY-2004 (First entry)  
**Human ovarian specific polypeptide** SEQ ID NO:357.  
 KW Human; tumour necrosis factor receptor 2 related protein variant;  
 KW TNF<sub>2</sub>PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;  
 KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;  
 KW asthma; ulcerative colitis.

human; ovarian; cytostatic; immunostimulant; vaccine; gene therapy;  
ovarian cancer; immune response; cancer.

XX PN WO2003012037-A2.  
XX DS  
XX Homo sapiens.  
XX

WO2004013311-A2.  
13-FEB-2003.  
XX

PP 24-JUL-2002; 2002WO-US023684.  
XX

PR 27-JUL-2001; 2001US-00917372.  
XX  
PA (TINCYT-). INCYTER GENOMICS INC

(DIADE-) DIADEXUS INC. XX  
CA CA PI Lal PG, Warren BA;

XX Macina RA, Salceda S, Liu C, Sun Y, Turner LR; XX DR WPI; 2003-256445/25.

WPI: 2004-169331/16. New ovarian specific nucleic acid, useful in identifying, diagnosing, and treating a disease or condition associated with increased TNF signaling e.g., cancer of the prostate, ovary, gallbladder, breast, liver or colon, or PT PT PT xx

monitoring, staging, imaging and treating ovarian cancer and non-cancerous disease states in ovarian tissue.

PT **rheumatoid arthritis**, asthma.  
XX

Claim 12, GPO TN NO 267, 506000. Document Disclosure; Fig 2A-C; 64pp; English.  
PS  
yy

The present invention describes human tumour necrosis factor receptor 2 related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic and immunosuppressive activities, and can be used in gene therapy. The TNFR2PV cDNA or protein sequences can be used for preparing a composition for treating a disease or condition associated with increased TNF signalling e.g., cancer of the prostate, ovary, gallbladder, brain, liver or colon, or inflammatory disorders, such as rheumatoid arthritis, asthma or ulcerative colitis. The present sequence represents a human TNFR2 related protein/Lirbeta amino acid sequence, which is given in comparison with human TNFR2PV in the exemplification of the present invention.

SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;

Best Local Similarity 100.0%; Pred. No. 2.8e-78;

Matches 197; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 SQPQAVPPYASENOTCRDQEKEYEPQRHICSSRCRPPGTYVSAKCSRIRDTCATCAENS 60

Db 28 SQPQAVPPYASENOTCRDQEKEYEPQRHICSSRCRPPGTYVSAKCSRIRDTCATCAENS 87

Qy 61 YNEHWNYLTICOLCRPCDMGLIEEIAPISTSKRKTQCCQPMFCAAWALEBTHCELLSD 120

Db 88 YNEHWNYLTICOLCRPCDMGLIEEIAPISTSKRKTQCCQPMFCAAWALEBTHCELLSD 147

Qy 121 CPPGTAEALKDVEYGKGNHFCVPKCKAGHONTSSPSARCPHTRCENQLVEAPGTAQSD 180

Db 148 CPPGTAEALKDVEYGKGNHFCVPKCKAGHONTSSPSARCPHTRCENQLVEAPGTAQSD 207

Qy 181 TTCKRNPLPLEPPEMSGT 197

Db 208 TTCKRNPLPLEPPEMSGT 224

**RESULT 6**  
 ABR40220 standard; protein; 435 AA.  
 ID ABR40220;  
 AC ABR40220;  
 DT 12-JUN-2003 (first entry)  
 XX Human genoxin.

XX Human; genoxin; antiarteriosclerotic; antidiabetic; hypotensive; XX antilipemic; anorectic; immunomodulator; cytostatic; anti-HIV; XX antiinflammatory; cardiot; cereoprotective; gene therapy; XX tumour necrosis factor receptor; TNFR; body mass; weight loss; obesity. XX HOMO sapiens.

FH Location/Qualifiers  
 FT Peptide 1..30  
 FT Protein /label= Signal\_Peptide

FT Domain 31..435 /label= Mature\_genoxin  
 FT Domain .227 /label= Extracellular\_domain

FT Domain 228..248 /label= Transmembrane\_domain  
 FT Domain 249..435 /label= Intracellular\_domain

XX WO2003011322-A1.  
 XX PD 13-FEB-2003.  
 XX FT 31-JUL-2002; 2002WO-IB003417.  
 XX PR 02-AUG-2001; 2001US-0309917B.  
 XX PA (GEST ) GENSET SA.

CC The present invention relates to a novel method for screening for an agonist or antagonist of Genoxin activity. The agonists/antagonists of the invention have antiarteriosclerotic, antidiabetic, hypotensive, antiinflammatory, anorectic, immunomodulator, cytostatic, anti-HIV, antiinflammatory, cardiot, and cereoprotective activity. The polypeptides of the invention may have a use in gene therapy, and act as tumour necrosis factor receptor (TNFR) agonists. The method is used to screen for an agonist or antagonist of Genoxin. The method is useful in metabolic research, particularly, in discovering compounds that modulate Genoxin activity or that reduce or increase body mass and maintain weight loss, and in preventing or treating obesity-related diseases or disorders such as hyperlipidaemia, atherosclerosis, heart disease, stroke, insulin-resistant diabetes or hypertension, or for preventing or treating disorders associated with excessive weight loss, such as cachexia, cancer -related weight loss, acquired immunodeficiency syndrome (AIDS)-related weight loss, chronic inflammatory disease-related weight loss, or anorexia. The present sequence represents the human genoxin of the invention.

XX Example 10; Page 33-34; 37pp; English.

The invention relates to a novel method for screening for an agonist or antagonist of Genoxin activity. The agonists/antagonists of the invention have antiarteriosclerotic, antidiabetic, hypotensive, antiinflammatory, anorectic, immunomodulator, cytostatic, anti-HIV, antiinflammatory, cardiot, and cereoprotective activity. The polypeptides of the invention may have a use in gene therapy, and act as tumour necrosis factor receptor (TNFR) agonists. The method is used to screen for an agonist or antagonist of Genoxin. The method is useful in metabolic research, particularly, in discovering compounds that modulate Genoxin activity or that reduce or increase body mass and maintain weight loss, and in preventing or treating obesity-related diseases or disorders such as hyperlipidaemia, atherosclerosis, heart disease, stroke, insulin-resistant diabetes or hypertension, or for preventing or treating disorders associated with excessive weight loss, such as cachexia, cancer -related weight loss, acquired immunodeficiency syndrome (AIDS)-related weight loss, chronic inflammatory disease-related weight loss, or anorexia. The present sequence represents the human genoxin of the invention.

XX Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-78;  
 Matches 197; Conservative 0; Mismatches 0; Gaps 0;

Qy	1 SQPQAVPPYASENOTCRDQEKEYEPQRHICSSRCRPPGTYVSAKCSRIRDTCATCAENS 60	Db	28 SQPQAVPPYASENOTCRDQEKEYEPQRHICSSRCRPPGTYVSAKCSRIRDTCATCAENS 87
Qy	61 YNEHWNYLTICOLCRPCDMGLIEEIAPISTSKRKTQCCQPMFCAAWALEBTHCELLSD 120	Qy	61 YNEHWNYLTICOLCRPCDMGLIEEIAPISTSKRKTQCCQPMFCAAWALEBTHCELLSD 120
Db	88 YNEHWNYLTICOLCRPCDMGLIEEIAPISTSKRKTQCCQPMFCAAWALEBTHCELLSD 147	Db	88 YNEHWNYLTICOLCRPCDMGLIEEIAPISTSKRKTQCCQPMFCAAWALEBTHCELLSD 147
Qy	121 CPPGTAEALKDVEYGKGNHFCVPKCKAGHONTSSPSARCPHTRCENQLVEAPGTAQSD 180	Qy	121 CPPGTAEALKDVEYGKGNHFCVPKCKAGHONTSSPSARCPHTRCENQLVEAPGTAQSD 180
Db	148 CPPGTAEALKDVEYGKGNHFCVPKCKAGHONTSSPSARCPHTRCENQLVEAPGTAQSD 207	Db	148 CPPGTAEALKDVEYGKGNHFCVPKCKAGHONTSSPSARCPHTRCENQLVEAPGTAQSD 207
Qy	181 TTCKRNPLPLEPPEMSGT 197	Qy	181 TTCKRNPLPLEPPEMSGT 197
Db	208 TTCKRNPLPLEPPEMSGT 224	Db	208 TTCKRNPLPLEPPEMSGT 224

Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-78;  
 Matches 197; Conservative 0; Mismatches 0; Gaps 0;

Qy	1 SQPQAVPPYASENOTCRDQEKEYEPQRHICSSRCRPPGTYVSAKCSRIRDTCATCAENS 60	Db	28 SQPQAVPPYASENOTCRDQEKEYEPQRHICSSRCRPPGTYVSAKCSRIRDTCATCAENS 87
Qy	61 YNEHWNYLTICOLCRPCDMGLIEEIAPISTSKRKTQCCQPMFCAAWALEBTHCELLSD 120	Qy	61 YNEHWNYLTICOLCRPCDMGLIEEIAPISTSKRKTQCCQPMFCAAWALEBTHCELLSD 120
Db	88 YNEHWNYLTICOLCRPCDMGLIEEIAPISTSKRKTQCCQPMFCAAWALEBTHCELLSD 147	Db	88 YNEHWNYLTICOLCRPCDMGLIEEIAPISTSKRKTQCCQPMFCAAWALEBTHCELLSD 147
Qy	121 CPPGTAEALKDVEYGKGNHFCVPKCKAGHONTSSPSARCPHTRCENQLVEAPGTAQSD 180	Qy	121 CPPGTAEALKDVEYGKGNHFCVPKCKAGHONTSSPSARCPHTRCENQLVEAPGTAQSD 180
Db	148 CPPGTAEALKDVEYGKGNHFCVPKCKAGHONTSSPSARCPHTRCENQLVEAPGTAQSD 207	Db	148 CPPGTAEALKDVEYGKGNHFCVPKCKAGHONTSSPSARCPHTRCENQLVEAPGTAQSD 207
Qy	181 TTCKRNPLPLEPPEMSGT 197	Qy	181 TTCKRNPLPLEPPEMSGT 197
Db	208 TTCKRNPLPLEPPEMSGT 224	Db	208 TTCKRNPLPLEPPEMSGT 224

RESULT 7  
 ABU89821 standard; protein; 435 AA.  
 ID ABU89821  
 AC ABU89821;  
 XX DT 10-JUL-2003 (first entry)  
 XX XX TNF-receptor associated Factor 5 (TRAF5) interacting protein #1.  
 XX Human; cytostatic; DAPK3-Agonist; cancer;  
 KW TNF-receptor associated Factor 5 interacting protein;  
 KW tumour necrosis factor associated Factor 5 interacting protein;  
 KW TRAF5 interacting protein.  
 XX OS Homo sapiens.  
 XX PN WO20030131571-A2.





ABM81346 ID ABM81346 standard; protein; 435 AA. XX	Db 88 YNEHWNLYTICQLCRPCDPVMGLEIAPTSKRKTOCQPMFCAAWALECTHCELSD 147
AC ABM81346; XX	Qy 121 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPASACQPHTRCENGCLVEAAPGTAQSD 180
DT 18-NOV-2004 (first entry) XX	Db 148 CPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPASACQPHTRCENGCLVEAAPGTAQSD 207
DB Tumour-associated antigenic target (TAT) polypeptide PRO2622, SEQ: 3477. XX	Qy 181 TRCKNPLIEPLPPMSGT 197
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer; KW tumour; diagnosis; cell proliferative disorder; breast cancer; KW colorectal cancer; lung cancer; ovarian cancer; liver cancer; KW central nervous system cancer; bladder cancer; pancreatic cancer; KW cervical cancer; melanoma; leukaemia; hybridisation probe; KW chromosome identification; chromosome mapping; gene mapping; KW gene therapy; cytostatic. XX	Db 208 TRCKNPLIEPLPPMSGT 224
OS Homo sapiens. XX	RESULTS 1.2 ABM81346 standard; protein; 439 AA. ID ABM81346; XX
PN WO2004030615-A2. XX	AC ABM81346; XX
PD 15-APR-2004. XX	DT 18-NOV-2004 (first entry) XX
PP 29-SEP-2003; 2003WO-US028547. XX	DE Human diagnostic and therapeutic pprotein SEQ ID NO:3860. XX
PR 02-OCT-2002; 2002US-0414971P. XX	KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp. XX
PA (GETH ) GENENTECH INC. XX	OS Homo sapiens. XX
PI Wu TD, Zhang Z, Zhou Y; XX	PN WO2004023973-A2. XX
DR WPI; 2004-347921/32. N-PSDB; ACN3374.	PD 25-MAR-2004. XX
PR New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor. XX	PP 12-SEP-2003; 2003WO-US028227. XX
PS Claim 12; SEQ ID NO 3477: "2273pp; English. XX	PR 12-SEP-2002; 2002US-0410259P. XX
CC The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides, expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention XX	PR 12-SEP-2002; 2002US-0410260P. XX
CC Sequence 435 AA; SQ Query Match 100.0%; Score 1133; DB 8; Length 435; Best Local Similarity 100.0%; Pred. No. 2..8e-7; Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PA (INCY-) INCYTE CORP. XX
Qy 1 SQPAVPPYASENOTCRDQEKEYEPQRICCSRCPPGTYSAKCSRDTVCATCAENS 60 DB 28 SQPAVPPYASENOTCRDQEKEYEPQRICCSRCPPGTYSAKCSRDTVCATCAENS 87 Qy 61 YNEHWNLYTICQLCRPCDPVMGLEIAPTSKRKTOCQPMFCAAWALECTHCELSD 120	PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; PI Harthasorne RA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; PI Mooney EM, Deleageane AM, Panesar IS, Banville SC, Reddy TP; PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH; PI Peralta CH, Anderson SB, Riojas P, Shem EJ, Wu MC, Stuve LL; PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D; PI Patury S, Shi X, Suarez CJ; PI WPI; 2004-329368/30. DR N-PSDB; ACN42263. XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune disorders, .9. cell proliferative disorders, .9. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at <a href="http://www.wipo.int/pct/en/sequences/listing.htm">www.wipo.int/pct/en/sequences/listing.htm</a>	PT New diagnostic and therapeutic polynucleotides and polypeptides, useful molecules e.g. autoimmune or inflammatory disorders, in gene therapy or in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmunity or inflammatory disorders and in gene mapping. XX
PS Claim 27; Page; 190pp; English. XX	PT PR in diagnosing a condition, disease or disorder associated with human molecules e.g. autoimmunity or inflammatory disorders and in gene mapping. XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, .9. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at <a href="http://www.wipo.int/pct/en/sequences/listing.htm">www.wipo.int/pct/en/sequences/listing.htm</a>	PS PR in diagnosing a condition, disease or disorder associated with human molecules e.g. autoimmunity or inflammatory disorders and in gene mapping. XX
Qy 1 SQPAVPPYASENOTCRDQEKEYEPQRICCSRCPPGTYSAKCSRDTVCATCAENS 60 DB 28 SQPAVPPYASENOTCRDQEKEYEPQRICCSRCPPGTYSAKCSRDTVCATCAENS 87 Qy 61 YNEHWNLYTICQLCRPCDPVMGLEIAPTSKRKTOCQPMFCAAWALECTHCELSD 120	CC

SQ Sequence 439 AA;

Query Match 100.0%; Score 1133; DB 8; Length 439;  
Best Local Similarity 100.0%; Pred. No. 2. 8e-78;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPYASENOTCRDQEKEYEPOHRICCSRCPPETYSAKCSRIRDTCATCAENS 60  
Db 28 SQPQAVPYASENOTCRDQEKEYEPOHRICCSRCPPETYSAKCSRIRDTCATCAENS 87

Qy 61 YNEHWNWNTLICOLCRPCDPVMGLIEAPOTSKRTQCCQPGMFCAAWALECTHCELLSD 120  
Db 88 YNEHWNWNTLICOLCRPCDPVMGLIEAPOTSKRTQCCQPGMFCAAWALECTHCELLSD 147

Qy 121 CPGTEALKDEVKGHNHCUPKAHGNTSSPSARCPHRCTCENQLVERAAGTAQSD 180  
Db 148 CPPTEALKDEVKGHNHCUPKAHGNTSSPSARCPHRCTCENQLVERAAGTAQSD 207

Qy 181 TTCKNPLBLPPMSGT 197  
Db 208 TTCKNPLBLPPMSGT 224

RESULT 13  
ID ABM83610  
OS Homo sapiens .  
AC ACB83610;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:3859.  
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp;  
OS Homo sapiens .  
XX PN WO2004023973-A2.  
XX PD 25-MAR-2004.  
XX PF 12-SEP-2003; 2003WO-US028227.  
XX PR 12-SEP-2002; 2002US-0410253P.  
PR 12-SEP-2002; 2002US-0410263P.  
XX PA (INCY-) INCYTE CORP.  
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
Mooney EM, Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
Mooney EM, Deleseane AM, Panesar IS, Banville SC, Reddy TP;  
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstlin EH;  
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Steve LL;  
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
Xu Y, Kwon M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
Patury S, Shi X, Suarez CJ;  
DR WPI: 2004-329368/30.  
XX N-FSDB; ACN12262.

New diagnostic and therapeutic polynucleotides and polypeptides, useful  
in diagnosing a condition, disease or disorder associated with human  
molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
in gene mapping.

Claim 27: Page: 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides  
selected from one of the 2722 sequences defined in the specification. A  
polynucleotide of the invention may have a use in gene therapy. The human  
diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
used to diagnose a particular condition, disease or disorder associated  
with human molecules, e.g. cell proliferative disorders,

SQ Sequence 446 AA;

Query Match 100.0%; Score 1133; DB 8; Length 446;  
Best Local Similarity 100.0%; Pred. No. 2. 8e-18;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPYASENOTCRDQEKEYEPOHRICCSRCPPGTVSAKCSRIRDTCATCAENS 60  
Db 28 SQPQAVPYASENOTCRDQEKEYEPOHRICCSRCPPGTVSAKCSRIRDTCATCAENS 87

Qy 61 YNEHWNWNTLICOLCRPCDPVMGLIEAPOTSKRTQCCQPGMFCAAWALECTHCELLSD 120  
Db 88 YNEHWNWNTLICOLCRPCDPVMGLIEAPOTSKRTQCCQPGMFCAAWALECTHCELLSD 147

Qy 121 CPPGTRAEELKDEVKGHNHCUPKAHGNTSSPSARCPHRCTCENQLVERAAGTAQSD 180  
Db 148 CPPGTRAEELKDEVKGHNHCUPKAHGNTSSPSARCPHRCTCENQLVERAAGTAQSD 207

Qy 181 TTCKNPLELPLPPMSGT 197  
Db 208 TTCKNPLELPLPPMSGT 224

RESULT 14  
ID ADJ67840  
OS Homo sapiens .  
AC ADJ67640 standard; protein; 450 AA.  
XX AC ADJ67640;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human ovarian specific polypeptide SEQ ID NO:354.  
XX KW human; ovarian; cytostatic; immunostimulant; vaccine; gene therapy;  
KW ovarian cancer; immune response; cancer.  
XX Homo sapiens .  
XX OS Homo sapiens .  
XX PN WO2004013311-A2.  
XX PD 12-FEB-2004.  
XX PF 06-AUG-2003; 2003WO-US024669.  
XX PR 06-AUG-2002; 2002US-0401469P.  
XX PA (DIAD-) DIADEXUS INC.  
XX PI Macina RA, Salceda S, Liu C, Sun Y, Turner LR;  
XX DR WPI: 2004-169331/16.  
PT New ovarian specific nucleic acid, useful in identifying, diagnosing,  
monitoring, staging, imaging and treating ovarian cancer and non-  
cancerous disease states in ovarian tissue.  
XX PT The invention relates to novel isolated ovarian specific nucleic acid  
molecules and the polypeptides encoded by them. A protein of the  
invention has cytostatic and immunostimulant activity. A nucleic acid of  
the invention may have a use as a vaccine, and in gene therapy. The  
XX PS Claim 12; SEQ ID NO 354; 586pp; English.  
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,

CC nucleic acid molecule or polypeptide, antibody or kit is useful in  
 CC identifying, diagnosing, monitoring, staging, imaging and treating  
 CC ovarian cancer and non cancerous disease states in ovarian tissue and in  
 CC inducing an immune response against the ovarian cancer cell. The  
 CC sequences shown in ADJ67535-ABJ67682 represent ovarian specific  
 CC polypeptides of the invention.

XX Sequence 450 AA;

Query	Match	Score 1133; DB 8; Length 450;
Best Local Similarity	100.0%;	Pred. No. 2.9e-78;
Matches	197;	Mismatches 0;
Conservative	0;	Indels 0;
		Gaps 0;

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  1 SQPQAVPPYASENQTCRDQKEYEPQRHICCSRCPGTVSAKCSRIRDTCATCAENS 60
  28 SQPQAVPPYASENQTCRDQKEYEPQRHICCSRCPGTVSAKCSRIRDTCATCAENS 87
  61 YNEHHNYLTICQLCRPCDPVNGLEIAAPCTSKRTQCRCPGMFCAAVALETCCELLSD 120
  88 YNEHHNYLTICQLCRPCDPVNGLEIAAPCTSKRTQCRCPGMFCAAVALETCCELLSD 147
  121 CPPOTBAELKDEVKGNNRHCPCKAGHQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
  148 CPPGTEAELKDEVGKGNNHCPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
  181 TTCKNPLBLPPPEMSGT 197
  208 TTCKNPLBLPPPEMSGS 224

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Search completed: September 23, 2005, 10:27:33  
 Job time : 75 secs

RESULT 15

ABP96136 standard; protein; 399 AA.

XX

AC ABP96136;

XX

DT 09-MAY-2003 (first entry)

XX Human TNF receptor 2 related protein variant SEQ ID NO:1.

XX Human; tumour necrosis factor receptor 2 related protein variant;

XX TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;

XX TNF signalling; cancer inflammatory disorder; rheumatoid arthritis;

XX asthma; ulcerative colitis.

OS Homo sapiens.

XX PN WO2003012037-A2.

XX PD 13-FEB-2003.

XX

PP 24-JUL-2002; 2002WO-US23684.

XX PR 27-JUL-2001; 2001US-00917372.

XX PA (INCYTE GENOMICS INC.

XX PI Lai PG, Warren BA;

XX DR WPI; 2003-255445/25.

XX N-PSDB; ABZ79717.

XX PT New cDNA, useful for preparing a composition for treating a disease or

PT condition associated with increased TNF signaling e.g., cancer of the

PT prostate, ovary, gallbladder, breast, brain, liver or colon, or

PT rheumatoid arthritis, asthma.

XX PS Claim 20; Fig 1A-F; 64pp; English.

XX The present sequence represents human tumour necrosis factor receptor 2  
 CC related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic  
 CC and immunosuppressive activities, and can be used in gene therapy. The  
 CC TNFR2PV cDNA or protein sequences can be used for preparing a composition

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2005, 09:52:51 ; Search time 43 Seconds  
(without alignments)

341.997 Million cell updates/sec

Title: US-10-077-406-1  
Perfect score: 1133  
Sequence: 1 SQQAVPPYASENQTCRDQE.....QSDTTCKNPLBPLPDEMSGT 197

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6\_ptodata/1/iaa/5A\_COMB.pep:  
2: /cgn2\_6\_ptodata/1/iaa/5B\_COMB.pep:  
3: /cgn2\_6\_ptodata/1/iaa/6A\_COMB.pep:  
4: /cgn2\_6\_ptodata/1/iaa/6B\_COMB.pep:  
5: /cgn2\_6\_ptodata/1/iaa/PCTUS\_COMB.pep:  
6: /cgn2\_6\_ptodata/1/iaa/backfile1.pep:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	197	2	US-08-505-606-1 Sequence 1, Appli
2	1133	100.0	197	4	US-09-000-166-1 Sequence 1, Appli
3	1133	100.0	197	4	US-09-303-262-1 Sequence 1, Appli
4	1133	100.0	473	4	US-09-949-016-7944 Sequence 7944, Appli
5	987	87.1	170	4	US-08-828-683A-14 Sequence 14, Appli
6	981	86.6	170	4	US-09-523-323-57 Sequence 57, Appli
7	771	68.0	415	3	US-09-006-353A-6 Sequence 6, Appli
8	771	68.0	415	4	US-09-573-986-6 Sequence 6, Appli
9	456	40.2	77	3	US-08-866-545-3 Sequence 3, Appli
10	456	40.2	77	4	US-09-627-775-3 Sequence 3, Appli
11	305	26.9	227	3	US-08-974-022-18 Sequence 48, Appli
12	305	26.9	227	3	US-08-795-445A-48 Sequence 48, Appli
13	305	26.9	227	3	US-08-447A-48 Sequence 48, Appli
14	305	26.9	227	3	US-08-974-186-48 Sequence 48, Appli
15	305	26.9	227	3	US-08-795-446B-48 Sequence 48, Appli
16	305	26.9	227	3	US-08-705-945D-134 Sequence 134, Appli
17	305	26.9	227	4	US-08-577-188C-48 Sequence 48, Appli
18	305	26.9	235	3	US-09-326-394-4 Sequence 4, Appli
19	305	26.9	235	4	US-09-580-235-2 Sequence 2, Appli
20	305	26.9	235	4	US-09-580-235-8 Sequence 8, Appli
21	305	26.9	235	4	US-09-580-181-2 Sequence 2, Appli
22	305	26.9	235	4	US-09-580-181-8 Sequence 8, Appli
23	305	26.9	235	4	US-09-102-530-2 Sequence 2, Appli
24	305	26.9	235	4	US-09-102-530-8 Sequence 8, Appli
25	305	26.9	235	4	US-09-579-845-10 Sequence 10, Appli
26	305	26.9	461	1	US-08-385-229-2 Sequence 2, Appli
27	305	26.9	461	2	US-08-650-000-2 Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-08-505-606-1  
; Sequence 1, Application US/08505606  
; Patent No. 5923351

; GENERAL INFORMATION:

; APPLICANT: BROWNING, Jeffrey L.  
; APPLICANT: BENJAMIN, Christopher D.  
; APPLICANT: HOCHMAN, Paula S.  
; TITLE OF INVENTION: SOLUBLE LIMPHOTOXIN-BETA RECEPTORS AND ANTI-LIMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL DISEASE

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr.  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10020

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/505,606  
; FILING DATE: 21-JUL-1995  
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/378,968  
; FILING DATE: 26-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HALEY, Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B191

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367

; INFORMATION FOR SEQ ID NO: 1:  
; SEQENCE CHARACTERISTICS:  
; LENGTH: 197 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear

; MOLECULE TYPE: peptide

Query Match 100.0%; Score 1133; DB 2; Length 197;



CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 20/012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 7944  
; LENGTH: 473  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-949-016-7944

Query Match Score 100.0%; Score 1133; DB 4; Length 473;  
Best Local Similarity 100.0%; Pred. No. 9e-99; Mismatches 0; Indels 0; Gaps 0;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQQAVPPAYSENQTCRDQEKEYEPQRICRCPPGTYSAKCSRDTVCATCAENS 60  
Db 66 SQQAVPPAYSENQTCRDQEKEYEPQRICRCPPGTYSAKCSRDTVCATCAENS 125

Qy 61 YNEHWNLYTICOLCRPCDPVMGLIEIACTSKRKTKOCCRQCPGMFCAAWALECTHCELLS 120  
Db 126 YNEHWNLYTICOLCRPCDPVMGLIEIACTSKRKTKOCCRQCPGMFCAAWALBCTHCBLLSD 185

Qy 121 CPPCTEAKLDEYGKGNHCVPCKAGHQNTSSPSARCPQHTRCENQLVEAAPGTAQSD 180  
Db 186 CPPCTEAKLDEYGKGNHCVPCKAGHQNTSSPSARCPQHTRCENQLVEAAPGTAQSD 245

Qy 181 TTCKNPLBLPPMSGT 197  
Db 246 TTCKNPLBLPPMSGT 262

RESULT 5  
US-08-828-683A-14  
; Sequence 14, Application US/08828683A  
; Patent No 6469144-  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,683A  
FILING DATE: 31-Mar-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/625328  
FILING DATE: 1-Apr-1996  
APPLICATION NUMBER: 08/710802  
FILING DATE: 23-Sep-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1007P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-3981  
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 170 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-08-828-683A-14

Query Match Score 87.1%; Score 987; DB 4; Length 170;  
Best Local Similarity 100.0%; Pred. No. 1.6e-85; Mismatches 0; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TCRDQEKEYEFQHRICCSRCBPGBTVSACKCSRDTVCATCAENSYNEHWNLYTICQLC 74  
Db 1 TCRDQEKEYEFQHRICCSRCBPGBTVSACKCSRDTVCATCAENSYNEHWNLYTICQLC 60

Qy 75 RPPCDPMLGLEIACTSKRKTKOCCRQCPGMFCAAWALECTHCELLS 134  
Db 61 RPPCDPMLGLEIACTSKRKTKOCCRQCPGMFCAAWALECTHCELLS 120

Qy 135 KGNHCVPCPKAGHQNTSSPSARCPQHTRCENQLVEAAPGTAQSDTTCK 184  
Db 121 KGNHCVPCPKAGHQNTSSPSARCPQHTRCENQLVEAAPGTAQSDTTCK 170

RESULT 6  
Sequence 57, Application US/09523323  
; Patent No 6635743-  
GENERAL INFORMATION:  
APPLICANT: Boner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M.  
APPLICANT: Ulrich, Stephan  
APPLICANT: Zhai, Yifan  
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
FILE REFERENCE: 1488.065000C  
CURRENT APPLICATION NUMBER: US/09/523,323  
CURRENT FILING DATE: 2000-03-10  
EARLIER APPLICATION NUMBER: 60/168,380  
EARLIER FILING DATE: 1999-12-02  
EARLIER APPLICATION NUMBER: 60/148,326  
EARLIER FILING DATE: 1999-08-11  
EARLIER APPLICATION NUMBER: 60/142,657  
EARLIER FILING DATE: 1999-07-06  
EARLIER APPLICATION NUMBER: 60/137,457  
EARLIER FILING DATE: 1999-06-04  
EARLIER APPLICATION NUMBER: 60/124,041  
EARLIER FILING DATE: 1999-03-11  
EARLIER APPLICATION NUMBER: 09/252,656  
EARLIER FILING DATE: 1999-02-19  
EARLIER APPLICATION NUMBER: 60/075,409  
EARLIER FILING DATE: 1998-02-20  
EARLIER APPLICATION NUMBER: 09/027,287  
EARLIER FILING DATE: 1998-02-20  
EARLIER APPLICATION NUMBER: 09/003,886  
EARLIER FILING DATE: 1998-01-07  
EARLIER APPLICATION NUMBER: 08/822,953  
EARLIER FILING DATE: 1997-03-21  
EARLIER APPLICATION NUMBER: 60/013,923  
EARLIER FILING DATE: 1996-03-22  
EARLIER APPLICATION NUMBER: 60/030,157  
EARLIER FILING DATE: 1996-10-31  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 57  
LENGTH: 170  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (7)  
OTHER INFORMATION: May be any amino acid

US-09-523-323-57

Query Match 86.6%; Score 981; DB 4; Length 170;  
 Best Local Similarity 99.4%; Pred. No. 6e-85; Indels 0; Gaps 0;  
 Matches 169; Conservative 0; Mismatches 1; Gaps 0;

Qy 15 TCRQEQEYEPQRICCSRCPPTVSAKCSRRTDTVCATCAENSTBEHWNYLTICOLC 74  
 Db 1 TCRQEQEYEPQRICCSRCPGTYVSAKCSRRTDTVCATCAENSTBEHWNYLTICOLC 60

RESULT 8  
 US-09-573-986-6  
 Sequence 6, Application US/09573986  
 ; GENERAL INFORMATION:  
 ; Patent No. 6455040  
 ; APPLICANT: Wei, Ying-Fei  
 ; NI, Jian  
 ; APPLICANT: Gentz, Reiner  
 ; APPLICANT: Ruben, Steven  
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
 ; FILE REFERENCE: 1488-128004  
 ; CURRENT APPLICATION NO.: US/09/573,986  
 ; CURRENT FILING DATE: 2000-05-18  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 415  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-573-986-6

Query Match 68.0%; Score 771; DB 4; Length 415;  
 Best Local Similarity 70.7%; Pred. No. 9.7e-65;  
 Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

Qy 1 KGNHHCVPKCKAGHFONTSSPARQPHTRCENGVLVEAAPGTAQSDTICK 184  
 Db 1 KGNHHCVPKCKAGHFONTSSPARQPHTRCENGVLVEAAPGTAQSDTICK 170

RESULT 7  
 US-09-006-353A-6  
 Sequence 6, Application US/09006353A  
 ; GENERAL INFORMATION:  
 ; Patent No. 6261801  
 ; COMPUTER READABLE FORM:  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patient Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/006, 353A  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROOKS, ANDERS A  
 ; REGISTRATION NUMBER: 36,373  
 ; REFERENCE/DOCKET NUMBER: PF341  
 ; TELECOMMUNICATION: (301) 309-8504  
 ; TELEFAX: (301) 309-8512  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 415 amino acids  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-006-353A-6

Query Match 68.0%; Score 771; DB 3; Length 415;  
 Best Local Similarity 70.7%; Pred. No. 9.7e-65; Indels 2; Gaps 1;  
 Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

Qy 1 SQQAVPPYASENOTCRDQEKEYEPQRICCSRCPPTVYSAKCSRRTDTVCATCAENS 60  
 Db 28 SQQLVPYRINTCWDQDKEYPMHDVCCSRCPGEFYFAVCSRSQDTVKCKTPHNS 87

RESULT 9  
 US-08-866-545-3  
 Sequence 3, Application US/08866545  
 ; GENERAL INFORMATION:  
 ; Patent No. 625535  
 ; APPLICANT: Greene, Mark I.  
 ; APPLICANT: Murali, Ramachandran  
 ; APPLICANT: Takasaki, Wataru  
 ; TITLE OF INVENTION: PEPTIDES AND PEPTIDE ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR CORRESPONDENCE ADDRESS:  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10036-2811  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette

Qy 61 YNEHWNLYTICOLCRPCPVMGLEEIAPTSRKTQCRCPGMFCAAWALETHC- ELL 118  
 Db 88 YNEHWNHLSTCQLCRPCDIVGFEEVAPCTSDRKAECQCPGMSCVYLDNECVHCBERL 147

Query Match 68.0%; Score 771; DB 3; Length 415;  
 Best Local Similarity 70.7%; Pred. No. 9.7e-65; Indels 2; Gaps 1;  
 Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

Qy 1 SQQAVPPYASENOTCRDQEKEYEPQRICCSRCPPTVYSAKCSRRTDTVCATCAENS 60  
 Db 28 SQQLVPYRINTCWDQDKEYPMHDVCCSRCPGEFYFAVCSRSQDTVKCKTPHNS 87

Qy 61 YNEHWNLYTICOLCRPCPVMGLEEIAPTSRKTQCRCPGMFCAAWALETHC- ELL 118  
 Db 88 YNEHWNHLSTCQLCRPCDIVGFEEVAPCTSDRKAECQCPGMSCVYLDNECVHCBERL 147

COMPUTER: IBM Compatible  
 SOFTWARE: FastSEQ Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/866,545  
 FILING DATE: 30-MAY-1997  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION NUMBER:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A  
 REFERENCE NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 009113-0004-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEFAX: 650-493-5556  
 TELEX: 66141 PENNIE  
 SEQUENCE FOR SEQ ID NO: 3  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 77 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 6265535e  
 US-08-866-545-3

Query Match 40.2% Score 456; DB 3; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 7e-36;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VCATCAENSYNEHNYNLITICOLCRPCDPVMGLBEIAPTSKRKTQCRQGMFCAAWALE 111  
 Db 1 VCATCAENSYNEHNYNLITICOLCRPCDPVMGLBEIAPTSKRKTQCRQGMFCAAWALE 60

Qy 112 CTHCELLSDCPPGTEAE 128  
 Db 61 CTHCELLSDCPPGTEAE 77

RESULT 10  
 US-09-627-775-3  
 Sequence 3, Application US/09627775  
 GENERAL INFORMATION:  
 APPLICANT: Greene, Mark  
 APPLICANT: Murali, Ramachandran  
 APPLICANT: Aoki, Kazuhiko  
 APPLICANT: Baron, Roland  
 TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis  
 FILE REFERENCE: UPN3832  
 CURRENT FILING DATE: 2000-07-28  
 PRIOR APPLICATION NUMBER: 60/146,090  
 PRIOR FILING DATE: 1999-07-28  
 NUMBER OF SEQ ID NOS: 29  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 77  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-627-775-3

Query Match 40.2% Score 456; DB 4; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 7e-36;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VCATCAENSYNEHNYNLITICOLCRPCDPVMGLBEIAPTSKRKTQCRQGMFCAAWALE 111  
 Db 1 VCATCAENSYNEHNYNLITICOLCRPCDPVMGLBEIAPTSKRKTQCRQGMFCAAWALE 60

Qy 112 CTHCELLSDCPPGTEAE 128

Db 61 CTHCELLSDCPPGTEAE 77

RESULT 11  
 US-08-974-022-48  
 Sequence 48, Application US/08974022  
 Patent No. 6015938  
 GENERAL INFORMATION:  
 APPLICANT: Boyle, William J.  
 APPLICANT: Lacey, David L.  
 APPLICANT: Calzone, Frank J.  
 APPLICANT: Chang, Ming-Shi  
 TITLE OF INVENTION: OSTEOPROTEGERIN  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Augen Inc.  
 STREET: 1840 Dehavenland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: USA  
 ZIP: 91320-1789  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/974,022  
 FILING DATE: 12-DEC-1995  
 CLASSIFICATION:  
 INFORMATION FOR SEQ ID NO: 48:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/577,788  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE DOCKET NUMBER: A-378  
 INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 227 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-974-022-48

Query Match 26.9% Score 305; DB 3; Length 227;  
 Best Local Similarity 35.0%; Pred. No. 3.9e-21;  
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

Qy 5 AVPPYASE-NOTCRDQEKEYEPQRHICCSRCPPGTVUSAKCSRIRDVTCACTCAENSYNE 63  
 Db 28 APTPYAPEPGSTCR--LREYYDTQTAQMCCSRSRCSPGHQAKVFTKTSDTVDSCEDSTYQ 85

Qy 64 HNLYLTICQLCR--PDPVMGLBEIAPTSKRKTQCRQGMFCAAWALE-CTHCCELLS 119  
 Db 86 LRNWVPBCLSGSRCSSDQV---ETOACTREONRRICTCFCGWYCALSKOBSCRCLAPL 141

Qy 120 DCPPG----TEAELKDEVGKCNHCVPCRAFHQTSSPSARCPTRCENQLYVERAP 174  
 Db 142 KCRPQFGVARPOTETSVV---CKPCKAPTSFSNTISSIDCRPHQICN---VVAIP 191

Qy 175 GTAQSDDTC--KNPLBLPP 192  
 Db 192 GNASRDAVCTSTSPTRSMAP 211

RESULT 12  
 US-08-795-445A-48  
 Sequence 48, Application US/08795445A  
 Patent No. 6284485  
 GENERAL INFORMATION:  
 APPLICANT: Boyle, William J.  
 APPLICANT: Lacey, David L.

APPLICANT: Calzone, Frank J.  
 APPLICANT: Chang, Ming-Shi  
 TITLE OF INVENTION: OSTEOPROTEGERIN  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amgen Inc.  
 STREET: 1840 Dehavenland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: USA  
 ZIP: 91320-1789  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/795,447A  
 FILING DATE: 08/07/95  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE/DOCKET NUMBER: A-378D2  
 INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 227 amino acids  
 TYPE: amino acid  
 STRANDBEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-795-447A-48

Query Match 26.9%; Score 305; DB 3; Length 227;  
 Best Local Similarity 35.0%; Pred. No. 3.9e-21;  
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

Qy 5 AVPPYASE-NQTCRDQEKEYYEPHQHICRCSRCPPGTVSAKCSRIRDIVCATCAENSYNE 63  
 Db 28 AFTPYAPEPGSTCR-LREYDDQTAQMCCSKCSPGQAHVKFCTKTSUTVCDSCEDSTYQ 85

Qy 64 HNNYLTCOLCR--PCDPYVMGLEETIAPCTSKRKTOCRGFMFCAWALE-CTHCELLS 119  
 Db 86 LMNWVPECLSGRCSSDQV---ETQACTEQNRIOTCRGWICLASKOEGCRLCPLR 141

Qy 120 DCPPG----TEAELKDDEVGKGNHHCVPKAGHFONTSSPSARCPHTRCENQGLVEAAP 174  
 Db 142 KCRPGFGVARPDTETSDVV-----CKCAPGTFSNTTSSTDICRHQICN---VVAIP 191

Qy 175 GTAQSDTTC-KNPLEPLPP 192  
 Db 192 GNASRDAVCTSTSPTRSMAP 211

RESULT 14  
 US-08-795-445A-48

Query Match 26.9%; Score 305; DB 3; Length 227;  
 Best Local Similarity 35.0%; Pred. No. 3.9e-21;  
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

Qy 64 HNNYLTCOLCR--PCDPYVMGLEETIAPCTSKRKTOCRGFMFCAWALE-CTHCELLS 119  
 Db 86 LMNWVPECLSGRCSSDQV---ETQACTEQNRIOTCRGWICLASKOEGCRLCPLR 141

Qy 120 DCPPG----TEAELKDDEVGKGNHHCVPKAGHFONTSSPSARCPHTRCENQGLVEAAP 174  
 Db 142 KCRPGFGVARPDTETSDVV-----CKCAPGTFSNTTSSTDICRHQICN---VVAIP 191

Qy 175 GTAQSDTTC-KNPLEPLPP 192  
 Db 192 GNASRDAVCTSTSPTRSMAP 211

RESULT 13  
 US-08-795-447A-48

Sequence 48, Application US/08795447A  
 Patent No. 6284728  
 GENERAL INFORMATION:  
 Boyle, William J.  
 Lacey, David L.  
 Calzone, Frank J.  
 Chang, Ming-Shi  
 TITLE OF INVENTION: OSTEOPROTEGERIN  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amgen Inc.  
 STREET: One Amgen Center Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: USA

Address: Amgen Inc.  
 Street: 1840 Dehavenland Drive  
 City: Thousand Oaks  
 State: California  
 Country: USA  
 Zip: 91320-1789

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/974,186  
 FILING DATE:  
 CLASSIFICATION:  
 APPLICATION NUMBER: 08/577,788  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE/DOCKET NUMBER: A-378  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 227 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-974-186-48

Query Match 26.9%; Score 305; DB 3; Length 227;  
 Best Local Similarity 35.0%; Pred. No. 3.9e-21;  
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;  
 Query 5 AVPPYASE-NOTCRDQEKEYEPOHRICCSRCRPGTYVSAKCSRIRDTCATCAENSYNE 63  
 Db 28 AFTPYAAPPGSTCR--LREYYDQTAQMCSCSKCSEQHQAKVFCFKTTSDFVCDSEDTYQ 85  
 Query 64 HNNYLTCOLCR--PCDPVMGLEBLAPCTSKRKTOCQPMFCAAWALE-CTHCBL 119  
 Db 86 LMNWVPECLSGSRCSSDQV----ETQACTREQNRICTCRPGWYCALSKOEGCRLCPLR 141  
 Query 120 DCPG----TEABLKDVEKGKGNNHCVPKAGHFONTSSPSARCPHTRCENQGLYRAAP 174  
 Db 142 KCRPFGVARYPGETSDVV----CKPCAPGTFSNTSSTDICRPHQICN---WVAIP 191  
 Query 175 GTAQSDTTC--KNPLEPLPP 192  
 Db 192 GNAQRDAVCTSSTSPTRNAP 211  
 Search completed: September 23, 2005, 10:32:08  
 Job time: 45 sec(s)

RESULT 15  
 US-08-795-446B-48  
 Sequence 48, Application US/08795446B  
 Patent No. 6288032  
 GENERAL INFORMATION:  
 APPLICANT: Boyle, William J.  
 APPLICANT: Lacey, David L.  
 APPLICANT: Calzone, Frank J.  
 APPLICANT: Chang, Ming-Shi  
 TITLE OF INVENTION: OSTEOPROTEGERIN  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amgen Inc.

STREET: 1840 Dehavenland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: USA  
 ZIP: 91320-1789

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/795,446B

FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/577,768  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE/DOCKET NUMBER: A-378  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 227 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

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Qy 61 YNEHWNLYTICOLCRPCPVMGLIEAPCTSKRTQCRCPGMFCAAWALECTCELLSD 120  
 Db 61 YNEHWNLYTICOLCRPCPVMGLIEAPCTSKRTQCRCPGMFCAAWALECTCELLSD 120  
 Qy 121 CPPGTEAELKDEVGKGNNHCVPKAGHFONTSSPSARCOPTRCENQGLVEAAPGTAQSD 180  
 Db 121 CPPGTEAELKDEVGKGNNHCVPKAGHFONTSSPSARCOPTRCENQGLVEAAPGTAQSD 180  
 Qy 181 TTCKNPLEPLPPMSGT 197  
 Db 181 TTCKNPLEPLPPMSGT 197

RESULT 2  
 US-10-077-406-1  
 Sequence 1, Application US/10077406  
 Publication No. US20050037003A1  
 GENERAL INFORMATION:  
 APPLICANT: Browning, et al.  
 TITLE OF INVENTION: Soluble Lymphotoxin-B Receptors and Anti-lymphotoxin  
 Receptor and Ligand Antibodies, as Therapeutic Agents  
 TITLE OF INVENTION: Receptor and Ligand Antibodies, as Therapeutic Agents  
 FILE REFERENCE: B191  
 CURRENT APPLICATION NUMBER: US/10/077,406  
 CURRENT FILING DATE: 2002-02-15  
 PRIOR APPLICATION NUMBER: US/09/000,166  
 PRIOR FILING DATE: 1998-06-08  
 PRIOR FILING DATE: PC/T/US96/12010  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 197  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-10-077-406-1

Query Match 100.0%; Score 1133; DB 17; Length 197;  
 Best Local Similarity 100.0%; Pred No. 3 4e-86; Mismatches 0; Indels 0; Gaps 0;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOPOAVPYASENOTCRDQEKEYEPORRICCSRCPPGTYVSAKCSRIRDTCATCAENS 60  
 Db 1 SOPOAVPYASENOTCRDQEKEYEPORRICCSRCPPGTYVSAKCSRIRDTCATCAENS 60  
 Qy 121 CPPGTEAELKDEVGKGNNHCVPKAGHFONTSSPSARCOPTRCENQGLVEAAPGTAQSD 180  
 Db 121 CPPGTEAELKDEVGKGNNHCVPKAGHFONTSSPSARCOPTRCENQGLVEAAPGTAQSD 180  
 Qy 181 TTCKNPLEPLPPMSGT 197  
 Db 181 TTCKNPLEPLPPMSGT 197

RESULT 4  
 US-09-768-779A-6  
 Sequence 6, Application US/09768779A  
 Patent No. US2002127637A1  
 GENERAL INFORMATION:  
 APPLICANT: NI, JIAN MOORE, PAUL  
 TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
 STREET: 9410 KEY WEST AVENUE  
 CITY: ROCKVILLE  
 STATE: MD  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/768,779A  
 FILING DATE: 25-Jan-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/086,582  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KENLEY K. HOOVER  
 REGISTRATION NUMBER: 40,302  
 REFERENCE/DOCKET NUMBER: FF368PP  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8439  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 435 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-768-779A-6

Query Match 100.0%; Score 1133; DB 9; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-86;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPYASENOTCRDQEKEYTEPQRHICCSRCPGTYVSAKCSRIRDTCATCAENS 60  
 Db 28 SQPQAVPYASENOTCRDQEKEYTEPQRHICCSRCPGTYVSAKCSRIRDTCATCAENS 87

Qy \*61 YNEHHWNYLTICOLCRPCDPGMGLERIAPICTSKRKTQCRCPGMFCAAWALECTCELLSD 120  
 Db 88 YNEHHWNYLTICOLCRPCDPGMGLERIAPICTSKRKTQCRCPGMFCAAWALECTCELLSD 147

Qy 121 CPPGTEALKDEVKGNNHCVPCKAGHFONTSSPSARCOPIHRCENQGLVEAPGTQSD 180  
 Db 148 CPPGTEALKDEVKGNNHCVPCKAGHFONTSSPSARCOPIHRCENQGLVEAPGTQSD 207

Qy 181 TTCKNPLIEPLPPMSGT 197  
 Db 208 TTCKNPLIEPLPPMSGT 224

---

RESULT 5  
 US-09-917-372-19

; Sequence 19, Application US/09917372  
 ; Publication No. US20030066619A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lal, Preeti G.  
 ; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT  
 ; FILE REFERENCE: PC-0050 US  
 ; CURRENT APPLICATION NUMBER: US/09/917-372  
 ; CURRENT FILING DATE: 2002-09-09  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO: 19  
 ; LENGTH: 435  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: Incyte ID No. US20030066619A1 9339762  
 ; US-09-917-372-19

Query Match 100.0%; Score 1133; DB 10; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-86;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPYASENOTCRDQEKEYTEPQRHICCSRCPGTYVSAKCSRIRDTCATCAENS 60  
 Db 28 SQPQAVPYASENOTCRDQEKEYTEPQRHICCSRCPGTYVSAKCSRIRDTCATCAENS 87

Qy 61 YNEHHWNYLTICOLCRPCDPGMGLERIAPICTSKRKTQCRCPGMFCAAWALECTCELLSD 120  
 Db 88 YNEHHWNYLTICOLCRPCDPGMGLERIAPICTSKRKTQCRCPGMFCAAWALECTCELLSD 147

Qy 121 CPPGTEALKDEVKGNNHCVPCKAGHFONTSSPSARCOPIHRCENQGLVEAPGTQSD 180  
 Db 148 CPPGTEALKDEVKGNNHCVPCKAGHFONTSSPSARCOPIHRCENQGLVEAPGTQSD 207

Qy 181 TTCKNPLIEPLPPMSGT 197  
 Db 208 TTCKNPLIEPLPPMSGT 224

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RESULT 6  
 US-10-087-192-942

; Sequence 942, Application US/10087192  
 ; Publication No. US20020182586A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morris, David W.  
 ; APPLICANT: Engelhard, Eric K.  
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

Query Match 100.0%; Score 1133; DB 14; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-86;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPYASENOTCRDQEKEYTEPQRHICCSRCPGTYVSAKCSRIRDTCATCAENS 60  
 Db 28 SQPQAVPYASENOTCRDQEKEYTEPQRHICCSRCPGTYVSAKCSRIRDTCATCAENS 87

Qy 61 YNEHHWNYLTICOLCRPCDPGMGLERIAPICTSKRKTQCRCPGMFCAAWALECTCELLSD 120  
 Db 88 YNEHHWNYLTICOLCRPCDPGMGLERIAPICTSKRKTQCRCPGMFCAAWALECTCELLSD 147

QY 121 CPPGTEAELKDEVKGNNHCVCPCKAGHFONTSSPSARCOPTRCENQCLVEAAPGTAQSD 180  
 Db 148 CPPGTEAELKDEVKGNNHCVCPCKAGHFONTSSPSARCOPTRCENQCLVEAAPGTAQSD 207

QY 181 TTCKNPLLEPLPPEMSGT 197  
 Db 208 TTCKNPLLEPLPPEMSGT 224

---

RESULT 8  
 US-10-369-300-17  
 ; Sequence 1, Application US/10369300  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fraser, Christopher  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF  
 ; TITLE OF INVENTION: IMMUNE  
 ; TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY  
 ; FILE REFERENCE: 7853-255  
 ; CURRENT APPLICATION NUMBER: US/10/369,300  
 ; CURRENT FILING DATE: 2003-02-19  
 ; PRIOR APPLICATION NUMBER: 60/7558,463  
 ; PRIOR FILING DATE: 2002-02-19  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 17  
 ; LENGTH: 435  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-369-300-17

Query Match 100.0%; Score 1133; DB 15; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-86;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO: 133  
 LENGTH: 435

QY 1 SQOPAQPVYASENOTCRDQEKEYEPOHRICCSRCPPGTYSAKCSRIRDTCATCAENS 60  
 Db 28 SQOPAQPVYASENOTCRDQEKEYEPOHRICCSRCPPGTYSAKCSRIRDTCATCAENS 87

QY 61 YNEHWNYLTICOLCRPCDPVMGLIEAPICTSKRKTQCCPQGMFCAAWELETHCELLSD 120  
 Db 88 YNEHWNYLTICOLCRPCDPVMGLIEAPICTSKRKTQCCPQGMFCAAWELETHCELLSD 147

QY 121 CPPGTEAELKDEVKGNNHCVCPCKAGHFONTSSPSARCOPTRCENQCLVEAAPGTAQSD 180  
 Db 148 CPPGTEAELKDEVKGNNHCVCPCKAGHFONTSSPSARCOPTRCENQCLVEAAPGTAQSD 207

QY 181 TTCKNPLLEPLPPEMSGT 197  
 Db 208 TTCKNPLLEPLPPEMSGT 224

---

RESULT 9  
 US-10-262-445-133  
 ; Sequence 1, Application US/10262445  
 ; Publication No. US20040014058A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alsobrook II, John  
 ; APPLICANT: Burgess, Catherine  
 ; APPLICANT: Catterton, Elina  
 ; APPLICANT: Chant, John  
 ; APPLICANT: Chaudhuri, Amitabha  
 ; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Giot, Loic  
 ; APPLICANT: Gorman, Linda  
 ; APPLICANT: Guo, Xiaojia  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Mezes, Peter  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Ooi, Chean Eng

Query Match 100.0%; Score 1133; DB 15; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-86;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO: 133  
 LENGTH: 435

QY 61 YNEHWNYLTICOLCRPCDPVMGLEAPICTSKRKTQCCPQGMFCAAWELETHCELLSD 120  
 Db 88 YNEHWNYLTICOLCRPCDPVMGLEAPICTSKRKTQCCPQGMFCAAWELETHCELLSD 147

QY 61 SQOPAQPVYASENOTCRDQEKEYEPOHRICCSRCPPGTYSAKCSRIRDTCATCAENS 60  
 Db 28 SQOPAQPVYASENOTCRDQEKEYEPOHRICCSRCPPGTYSAKCSRIRDTCATCAENS 87

QY 61 YNEHWNYLTICOLCRPCDPVMGLEAPICTSKRKTQCCPQGMFCAAWELETHCELLSD 120  
 Db 88 YNEHWNYLTICOLCRPCDPVMGLEAPICTSKRKTQCCPQGMFCAAWELETHCELLSD 147

QY 121 CPPGTEAELKDEVKGNNHCVCPCKAGHFONTSSPSARCOPTRCENQCLVEAAPGTAQSD 180  
 Db 148 CPPGTEAELKDEVKGNNHCVCPCKAGHFONTSSPSARCOPTRCENQCLVEAAPGTAQSD 207

QY 181 TTCKNPLLEPLPPEMSGT 197  
 Db 208 TTCKNPLLEPLPPEMSGT 224

---

RESULT 10  
 US-09-907-372-1  
 ; Sequence 1, Application US/090907372  
 ; Patent No. US2009068242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lal, Preeti G.  
 ; APPLICANT: Warren, Bridget A.  
 ; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT  
 ; FILE REFERENCE: PC-0050 US  
 ; CURRENT APPLICATION NUMBER: US/09/907,372  
 ; CURRENT FILING DATE: 2001-07-27

NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: PERL Program  
 SEQ ID NO: 1  
 LENGTH: 399  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 OTHER INFORMATION: Incyte ID No. US20030068619A1 7497867CD1  
 US-09-907-372-1

Query Match 99.6%; Score 1129; DB 9; Length 399;  
 Best Local Similarity 99.5%; Pred. No. 1.5e-85;  
 Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPYASENOTCRDQEKEYEPOHRCICCSRCPGPITYVSAKCSRIRDTVCATCAINS 60  
 Db 28 SQPQAVPYASENOTCRDQEKEYEPOHRCICCSRCPGPITYVSAKCSRIRDTVCATCAINS 87

Qy 61 YNEHHNNYLTCQLCRPCDPINGLEEAPCTSKRKTQRCPGMFCAAWALECTCELLSD 120  
 Db 88 YNEHHNNYLTCQLCRPCDPVNGLEEAPCTSKRKTQRCPGMFCAAWALECTCELLSD 147

Qy 121 CPPGTEAELKDEVGRKNNHCVCPKAGHFQNTSSPARCOPHTRCENQGLVEAAPGTAQSD 180  
 Db 148 CPPGTEAELKDEVGRKNNHCVCPKAGHFQNTSSPARCOPHTRCENQGLVEAAPGTAQSD 207

Qy 181 TTCKNPLEPLPPPEMSGT 197  
 Db 208 TTCKNPLEPLPPPEMSGS 224

---

RESULT 11  
 US-09-917-372-1  
 Sequence 1, Application US/0917372  
 Publication No. US20030068619A1  
 GENERAL INFORMATION:  
 APPLICANT: Lal, Preeti G.  
 ATTORNEY: Warren, Bridget A.  
 TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT  
 FILE REFERENCE: PC-0050 US  
 CURRENT APPLICATION NUMBER: US/09/917,372  
 CURRENT FILING DATE: 2002-09-09  
 NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: PERL Program  
 SEQ ID NO: 1  
 LENGTH: 399  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 OTHER INFORMATION: Incyte ID No. US20030068619A1 7497867CD1  
 US-09-917-372-1

Query Match 99.6%; Score 1129; DB 10; Length 399;  
 Best Local Similarity 99.5%; Pred. No. 1.5e-85;  
 Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQPQAVPYASENOTCRDQEKEYEPOHRCICCSRCPGPITYVSAKCSRIRDTVCATCAINS 60  
 Db 28 SQPQAVPYASENOTCRDQEKEYEPOHRCICCSRCPGPITYVSAKCSRIRDTVCATCAINS 87

Qy 61 YNEHHNNYLTCQLCRPCDPVNGLEEAPCTSKRKTQRCPGMFCAAWALECTCELLSD 120  
 Db 88 YNEHHNNYLTCQLCRPCDPVNGLEEAPCTSKRKTQRCPGMFCAAWALECTCELLSD 147

Qy 121 CPPGTEAELKDEVGRKNNHCVCPKAGHFQNTSSPARCOPHTRCENQGLVEAAPGTAQSD 180  
 Db 148 CPPGTEAELKDEVGRKNNHCVCPKAGHFQNTSSPARCOPHTRCENQGLVEAAPGTAQSD 207

Qy 181 TTCKNPLEPLPPPEMSGT 197  
 Db 208 TTCKNPLEPLPPPEMSGS 224

---

RESULT 12  
 US-10-484-148-1  
 Sequence 16, Application US/10484148  
 Publication No. US20040248251A1  
 GENERAL INFORMATION:  
 APPLICANT: LAL, Preeti G.; HONCHELL, Cynthia D.; BARROSO, Ines;  
 ATTORNEY: FORSYTHE, Ian J.; CHANIA, Narinder K.;  
 ATTORNEY: TANG, Y.; TOM, BOROWSKY, Mark L.;  
 ATTORNEY: WARREN, Bridget A.;  
 ATTORNEY: THANGAVELU, Ravitha; GIBERZEN, Kimberly J.;  
 ATTORNEY: AZIMZAI, Yaida; LEE, Ernestine A.;  
 ATTORNEY: BAUGHN, Mariah R.; GORAY, Ann E.;  
 ATTORNEY: DUGGAN, Brendan M.; TRAN, Bao;  
 ATTORNEY: LI, Joana X.; RICHARDSON, Thomas W.;  
 ATTORNEY: ELLIOTT, Vicki S.; ZEBARJADIAN, Yeganeh;  
 ATTORNEY: TRAN, Uyen K.; YAO, Monique G.;  
 ATTORNEY: PEPPERSON, David P.; LUO, Wen  
 ATTORNEY: LEHR-MASON, Patricia M.

TITLE OF INVENTION: RECEPTORS AND MEMBRANE ASSOCIATED PROTEINS  
 FILE REFERENCE: PF-1082 USN  
 CURRENT APPLICATION NUMBER: US/10/484,148  
 CURRENT FILING DATE: 2004-01-15  
 PRIOR APPLICATION NUMBER: PCT/US02/22833  
 PRIOR FILING DATE: 2002-07-16  
 PRIOR APPLICATION NUMBER: US 60/306,020  
 PRIOR FILING DATE: 2001-07-17  
 PRIOR APPLICATION NUMBER: US 60/308,179  
 PRIOR FILING DATE: 2001-07-27  
 PRIOR APPLICATION NUMBER: US 60/309,702  
 PRIOR FILING DATE: 2001-08-02  
 PRIOR APPLICATION NUMBER: US 60/311,476  
 PRIOR FILING DATE: 2001-08-10  
 PRIOR APPLICATION NUMBER: US 60/311,718  
 PRIOR FILING DATE: 2001-08-10  
 PRIOR APPLICATION NUMBER: US 60/311,551  
 PRIOR FILING DATE: 2001-08-10  
 PRIOR APPLICATION NUMBER: US 60/314,798  
 PRIOR FILING DATE: 2001-08-24  
 PRIOR APPLICATION NUMBER: US 60/316,639  
 PRIOR FILING DATE: 2001-08-31  
 PRIOR APPLICATION NUMBER: US 60/317,996  
 PRIOR FILING DATE: 2001-09-07  
 NUMBER OF SEQ ID NOS: 46  
 SOFTWARE: PERL Program  
 SEQ ID NO: 16  
 LENGTH: 416  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 OTHER INFORMATION: Incyte ID No: 7497865CD1  
 US-10-484-148-16

Query Match 97.8%; Score 1108; DB 16; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-84;  
 Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VPPYASENQTCRDLQKEKEYEPOHRCICCSRCPGPITYVSAKCSRIRDTVCATCAENSYNHW 65  
 Db 14 VPPYASENQTCRDLQKEKEYEPOHRCICCSRCPGPITYVSAKCSRIRDTVCATCAENSYNHW 73

Qy 66 NYLTICOLCRPCDPVMGLBEIACTSKRKTQCRCPGMFCAAWALECTCELLSDCPGT 125  
 Db 74 NYLTICQLCRPCDPVMGLBEIACTSKRKTQCRCPGMFCAAWALECTCELLSDCPGT 133

Qy 126 EALKDDEVGKGNNHCVCPKAGHFQNTSSPARCOPHTRCENQSLVERAAPGTAQSDTICKN 185  
 Db 134 EAELKDEVGKGNNHCVCPKAGHFQNTSSPARCOPHTRCENQSLVERAAPGTAQSDTICKN 193

Qy 186 PLEPLPPPEMSGT 197  
 Db 208 TTCKNPLEPLPPPEMSGS 224

Db 194 PLEPLPPENSGT 205

RESULT 13  
US-10-112-793-14  
; Sequence 14, Application US/10112793  
; Publication No. US2002019729A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94090

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/112,793  
FILING DATE: 28-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,683A  
FILING DATE: 31-Mar-1997  
APPLICATION NUMBER: 08/625348  
FILING DATE: 1-Apr-1996  
APPLICATION NUMBER: 08/710802  
FILING DATE: 23-Sep-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1007P1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-5416  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 amino acids  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-112-793-14

Query Match Score 87%; DB 13; Length 170;  
Best Local Similarity 100.0%; Pred. No. 3.8e-4;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCRDQEKEYEPOHRICCSRCPGTYVSAKCSRIRDTCATCAENSYNEHNNYLTCQLC 74  
Qy 15 TCRDQE--KEYEPOHRICCSRCPGTYVSAKCSRIRDTCATCAENSYNEHNNYLTCQLC 72  
Db 1 TCRDQEKEYEPOHRICCSRCPGTYVSAKCSRIRDTCATCAENSYNEHNNYLTCQLC 60

Query Match Score 970; DB 15; Length 172;  
Best Local Similarity 98.3%; Pred. No. 1e-72;  
Matches 169; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Db 1 TCRDQEKEYEPOHRICCSRCPGTYVSAKCSRIRDTCATCAENSYNEHNNYLTCQLC 60

OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-10-375-680-57

Query Match Score 85.6%;  
Best Local Similarity 98.3%;  
Matches 169; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 15 TCRDQE--KEYEPOHRICCSRCPGTYVSAKCSRIRDTCATCAENSYNEHNNYLTCQLC 72  
Db 1 TCRDQEKEYEPOHRICCSRCPGTYVSAKCSRIRDTCATCAENSYNEHNNYLTCQLC 60

Query Match Score 73%;  
Best Local Similarity 98.3%;  
Matches 132; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 73 LCRPCDPVMGLBIACTSKRKTOCQPGMFCAAWALETCCELLSDCPGTEAKDE 132  
Db 61 LCRPCDPVMGLBIACTSKRKTOCQPGMFCAAWALETCCELLSDCPGTEAKDE 120

Query Match Score 133%;  
Best Local Similarity 98.3%;  
Matches 133; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 133 VGRGNHHCVPCKAHGFTONTSSPSARCPHTRCENGQLEVAAPGTAQSDTICK 184  
Db 121 VGRGNHHCVPCKAHGFTONTSSPSARCPHTRCENGQLEVAAPGTAQSDTICK 172

RESULT 15  
US-09-948-018-19

Sequence 19, Application US/09948018  
; Patent No. US2002015097A1  
; GENERAL INFORMATION:  
; APPLICANT: Theill et al.  
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF  
; FILE REFERENCE: 01017/37677  
; CURRENT APPLICATION NUMBER: US/09/948,018  
; CURRENT FILING DATE: 2001-09-05  
; PRIOR APPLICATION NUMBER: US 60/230,191  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 45  
; SEQ ID NO 19  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; SOFTWARE: Patent in version 3.1  
; PRT  
; US-09-948-018-19

Query Match Score 780; DB 9; Length 257;  
Best Local Similarity 100.0%; Pred. No. 8.7e-57;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EHWNYLTICQLCRPCDPVMGLEBIACTSKRKTOCQPGMFCAAWALETCCELLSDCP 122  
Qy 63 EHWNYLTICQLCRPCDPVMGLEBIACTSKRKTOCQPGMFCAAWALETCCELLSDCP 60

Query Match Score 68.8%;  
Best Local Similarity 100.0%;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EHWNYLTICQLCRPCDPVMGLEBIACTSKRKTOCQPGMFCAAWALETCCELLSDCP 60

Query Match Score 123%;  
Best Local Similarity 98.3%;  
Matches 123; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 123 PGTEAKLKDEYKGNNHCVPCKAGHFNTSSPSARCPHTRCENGQLEVAAPGTAQSDT 182  
Db 61 PGTEAKLKDEYKGNNHCVPCKAGHFNTSSPSARCPHTRCENGQLEVAAPGTAQSDT 120

RESULT 14  
US-10-375-680-57  
; Sequence 57, Application US/10375680  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; APPLICANT: Yu, Guo-Liang

Query Match Score 183%;  
Best Local Similarity 98.3%;  
Matches 183; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 183 CKNPLPLPPENSGT 197  
Db 121 CKNPLPLPPENSGT 135

Search completed: September 23, 2005, 10:33:18  
Job time : 66 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6				
<b>OM protein - protein search, using sw model</b>					
Run on:	September 23, 2005, 09:46:31 ; Search time 40 Seconds (without alignments) 473.868 Million cell updates/sec				
Title:	US-10-077-406-1				
Perfect score:	1133				
Sequence:	1 SQPQAVPPYASENQTCRDQE.....QSDTICKNPLEPLPPMSGT 197				
Scoring table:	BLOSUM62				
Searched:	283416 seqs, 96216763 residues				
Total number of hits satisfying chosen parameters: 283416					
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing: Minimum Match 0% Maximum Match 100%					
Listing first 45 summaries					
Database :	PIR 79;*: 1: pir1;*: 2: pir2;*: 3: pir3;*: 4: pir4;*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	435	2 154182	tumor necrosis fac
2	305	26.9	461	1 A35356	tumor necrosis fac
3	295	26.0	474	2 B38634	tumor necrosis fac
4	290	25.6	459	2 I48854	gene murine tumour
5	278	24.5	277	2 A60771	B-cell activation
6	243.5	21.5	305	2 A46476	B cell-associated
7	226.5	20.0	651	2 JC7705	death receptor-6 -
8	221.5	19.6	271	2 S122783	OX0 antigen precu
9	214.5	18.9	272	1 I48700	gene ox40 protein
10	210.5	18.6	455	1 GQHUT1	tumor necrosis fac
11	210	18.5	348	2 T28623	hypothetical prote
12	210	18.5	349	2 D36858	gene G4R protein -
13	207	18.3	349	2 D72175	G2R protein - vari
14	206	18.2	461	2 JC4302	tumor necrosis fac
15	201	17.7	277	2 I37552	OX40 homolog - hum
16	201	17.7	454	1 GQMST1	tumor necrosis fac
17	196	17.3	595	1 A42086	CD10 antigen precu
18	195.5	17.3	255	2 I38426	lymphocyte activat
19	189	16.7	325	2 B43692	T2 protein - rabbi
20	187.5	16.5	314	2 I37383	FAS soluble protei
21	184.5	16.3	461	1 GQRTT1	tumor necrosis fac
22	183.5	16.2	326	1 GQVZML	T2 protein - myxof
23	181	16.0	335	2 A40036	apoptosis-mediated
24	179.5	15.8	256	2 B32393	T-cell antigen 4-1
25	171.5	15.1	425	1 A26431	nerve growth facto
26	166	14.7	493	2 JC5486	membrane glycoprot
27	164	14.5	416	1 JN0006	nerve growth facto
28	162	14.3	327	2 A46484	apoptosis-mediated
29	148.5	13.1	427	1 GQHUN	nerve growth facto

## ALIGNMENTS

## RESULT 1

154182

tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence\_revision 24-May-1996

C:Accession: I54182

R.Baens, M.-J. Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P., Genomics 16, 214-218, 1993.

A:Title--Construction and evaluation of a hncDNA library of human 12p transcribed sequences

A:Reference number: I54182; PMID: 84352381;

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Cross references: UNIPROT: P36941; GB: L04270; NID: 9339761; PID: 9336751; PID: 933976

C:Genetics:

A:Gene: GDB: LTBR

A:Map position: 12p13.3-12p13.1

C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homol.

Query	Match	Score	Length	DB 2;	DB 3;
Qy	1 SQPQAVPPYASENQTCDQEKEYEPQRICCSRPPTVYSAKCSRIRDIVTCATCAENS	100.0%	100.0%	Pred. No. 5.8e-78	0;
Db	28 SQPQAVPPYASENQTCDQEKEYEPQRICCSRPPTVYSAKCSRIRDIVTCATCAENS	99.9%	99.9%	Mismatches 0;	Indels 0;
Qy	61 YNHWNLYTICQLCRPDPVMGLEIAPCTSRSRKTKQCRCPGMFCAAWALB7HCBLLSD	100.0%	100.0%	0;	Gaps 0;
Db	88 YNHWNLYTICQLCRPDPVMGLEIABCTSRKTKQCRCPGMFCAAWALECTHCBLLSD	99.9%	99.9%	0;	0;
Qy	121 CPGTEARLKDVEKGKNNHCVPCKAGHFQNTSSPARQPHTRCENGOLVEARPGTAQSD	100.0%	100.0%	0;	0;
Db	148 CPGTEARLKDVEKGKNNHCVPCKAGHFQNTSSPARQPHTRCENGOLVEARPGTAQSD	99.9%	99.9%	0;	0;

## RESULT 2

A35356

tumor necrosis factor receptor 2 precursor [validated] - human

C:Alternate name: 75K tumor necrosis factor receptor type 2

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999

C:Accession: A35356; A36475; A48416; A336007; B35010; I38094 R.J.Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.; Science 248, 1019-1023, 1990

A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and

A;Reference number: A35356; MUID:90260639; PMID:2160731  
A;Accession: A35356  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-461 <SMI>  
A;Cross-references: UNIPROT:P20333; GB: M3315; NID: 9189185; PIDN: AAA599229.1; PID: 9189186  
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwarz, P.E.; King, M.W.; Hale, K.K.; Squires,  
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
A;Reference number: A36475; MUID:91045991; PMID:2172983  
A;Accession: A36475  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-195, 'R', 197-461 <KOH>  
A;Cross-references: GB: M5594; GB: M30549; NID: 33977; PIDN: AAA36755.1; PID: 9339758  
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.  
Cytokine 2, 231-237, 1990  
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,  
A;Reference number: A48416; MUID:91370690; PMID:1966549  
A;Accession: A48416  
A;Status: preliminary  
A;Molecule type: mRNA; protein  
A;Residues: 23-461 <DEIN>  
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIPI:633371)  
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra  
A;Reference number: A36007; MUID:90349572; PMID:2166946  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
A;Cross-references: GB: M3587; NID: 9139751; PIDN: AAA6322.1; PID: 9339752  
R;Hoetscher, H.; Schleiger, B.-J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.  
J. Biol. Chem. 265, 2031-2038, 1990  
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec  
A;Accession: A23666; MUID:91056048; PMID:2173696  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 23-40, 65-69; 136-141, 300-306 <LOE>  
R;Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A;Reference number: A35010; MUID:90110215; PMID:2153136  
A;Accession: A35010  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 27-31 <ENG>  
R;Kühnert, P.; Kemper, O.; Wallach, D.  
Gene 150, 381-386, 1994  
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of  
A;Accession: I3804  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-37 <RES>  
A;Cross-references: EMBL:X80021; NID: 9666044; PIDN: CAA56324.1; PID: 9825701  
C;Genetics:  
A;Gene: GDB:TNNFR2  
A;Cross-references: GDB:125914; OMIM:191191  
A;Map position: 1p36.2-1p36.2  
A;Introns: 26/3  
A;Note: the list of introns is incomplete  
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo  
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F;1-22/Domain: signal sequence; fatatu predicted <SIG>  
F;23-416/Domain: tumor necrosis factor receptor type 2 #status experimental <MAT>  
F;40-76/Domain: NGF receptor repeat homology <NG1>  
F;78-119/Domain: NGF receptor repeat homology <NG2>  
F;120-162/Domain: NGF receptor repeat homology <NG3>  
F;164-201/Domain: NGF receptor repeat homology <NG4>

F;262-279/Domain: transmembrane #status predicted <TMN>  
F;280-461/Domain: intracellular #status Predicted <INT>  
F;171-193/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 26.9%; Score 305; DB 1; Length 461;  
Best Local Similarity 35.0%; Pred. No. 7.e-16;  
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;  
QY 5 AVPYASB-NOTCRDQEKEYEPQRICCSRCPPGTYSAKCSRIRDTCATCAENSYNE 63  
Db 28 APTPYAPBPGSTCR -IREYYDQTAQMCCSCKSPGHAKVCTKTSDTVCDSEDTYQ 85  
QY 64 HNNYLTICQLCR--PCDPYNGLEETAPCTSKRKTKOQCOPGMPCAAWALB-CTHCBLLS 119  
Db 86 LMNWVPECLSCSSRSSDQV ---LEQACTREQNRICTCRGWCALSKQGCRLLAPLR 141  
QY 120 DCPPG---TEAELKDEVKGNNHCVCPKAGHQNTSSPARCPHTRCENQLYEAP 174  
Db 142 KCRPQFGVARPGETSDVV ---CKPQAGTFSNTTSSTDICRHQICN---VVAIP 191  
QY 175 GQAQSDFTC--KNPLBLPP 192  
Db 192 GNASMDAVCTSTSPTSMSMAP 211  
RESULT 3  
A;Cross-references: UNIPROT:P25119; GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:9199828  
R;Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.R.; Copeland, N.G.; Jenk  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor  
A;Reference number: A38634; MUID:91187895; PMID:1849278  
A;Accession: B38634  
A;Molecule type: mRNA  
A;Residues: 1-474 <IEW>  
A;Cross-references: GB: M60469; NID: 9199827; PIDN: AAA39752.1; PID: 9199828  
R;Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.R.; Copeland, N.G.; Jenk  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.  
A;Reference number: A40254  
A;Accession: A40254  
A;Molecule type: mRNA  
A;Residues: 1-474 <GOO>  
A;Cross-references: GB: M60469; NID: 9199827; PIDN: AAA39752.1; PID: 9199828  
R;Kissnerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovska, Y.  
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
A;Reference number: A40254; MUID:91246168; PMID:1645445  
A;Accession: A40254  
A;Molecule type: DNA  
A;Residues: 1-22 <ENG>  
A;Cross-references: EMBL:X87128; PIDN: CAA6018.1; PID: 9809044  
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo  
C;Keywords: cytokine receptor; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F;40-77/Domain: NGF receptor repeat homology <NG1>  
F;79-120/Domain: NGF receptor repeat homology <NG2>  
F;166-203/Domain: NGF receptor repeat homology <NG4>  
Query Match 26.0%; Score 295; DB 2; Length 474;  
Best Local Similarity 34.0%; Pred. No. 4.4e-15;  
Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;  
QY 8 PYASB-NOTCRDQEKEYEPQRICCSRCPPGTYSAKCSRIRDTCATCAENSYNEHWN 66  
Db 31 PYKPEPSYECQISQ-EYDRAQMCCRAKCPGQYYRHFNCNTSDDTVCADSFMSMTQVWN 89  
QY 67 YLTICQLCR--PCDPYNGLEETAPCTSKRKTKOQCOPGMPCAAWALB-CTHCBLLS 121

Db	90 QFPITCLSSSCTDQV---EIRACTKQNRVCAEAGRYCALTKHGSRCMRSLSKC 145	A; Experimental source: Burkitt lymphoma cell line Raji C; Gene: GDB:CD40 A; Cross-references: GDB:215268; OMIM:109355
Qy	122 PPGTEAELKDEVGKGNNNCVPCKAGHFTQNTSSSARCPHTRCENQIIVRAAPGTAQSDT 181	A; Map position: 20q12-20q13.2 C; Superfamily: CD27 antigen; NGF receptor repeat homology C; Keywords: B-cell; Glycoprotein; phosphoprotein; surface antigen; transmembrane protein
Db	146 GPSP-GVASSRAPNGNVTLCKACAPGTFSTDTDVPHRCS---ILATPGNASTDA 200	P:1-20/Domain: signal sequence #status predicted <SIG> P:21-277/Product: B-cell activation protein CD40 #status experimental <EXT> P:21-193/Domain: extracellular #status predicted <EXT> P:194-215/Domain: transmembrane #status predicted <TM> P:216-277/Domain: intracellular #status predicted <CYT>
Qy	182 TCKNPLBLPPMNS 195	P:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
Db	201 VC---ABESPTL 210	
<b>RESULT 4</b>		
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)		
C; species: Mus musculus (house mouse)		Query Match 24-5*: Score 278; DB 2; Length 277;
C; date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004		Best Local Similarity 35.0%; Pred. No. 5.5e-14;
C; accession: I48854		Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;
R; Powell, E.B.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.		
Mamm. Genome 5, 126-127, 1994		Qy 7 PPYASENOTCRDQEKEYEPQRHICCSRCRCPGTYVSAKCSRIRDTCATCAENSYNEHWN 66
A; Reference number: I48854		Db 22 PPVA----CR-EKOYLINSO--CCSNLCPQEGKLVSDCPTETECIPCGSEBEFLDTW 72
A; Accession: I48854		
A; Status: preliminary; translated from GB/EMBL/DBJ		Qy 67 YLTICQLCRPDPVMGLEBIAPTSKRKTQCRKQCPGMFCAAVALCPTCBLUSDCPPETE 126
A; Molecule type: mRNA		Db 73 RETHCHQHKYCDBNLGLVRVQKGTSERTDTCTCEGHFTCTSEA--CESCVLHRSCSPOFG 130
A; Residues: 1-459 <RES>		
A; Cross-references: UNIPROT:Q62327; EMBL:X76401; NID:9433830; PID:CAA53981.1; PID:943388		Qy 127 AE1KDEYGKGNHHCVPCPKAGHFONTSSPSARCPHTRCENQIIVRAAPGTAQSDTTC 183
C; Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog		Db 131 VK-QIATGVSDTICPEPVGFPSNVSSAFKCHPWTSCETKDLVVOAGTNKTDVV 186
F:151-188/Domain: NGF receptor repeat homology <NGF>;		
<b>RESULT 6</b>		
Query Match 25-6*: Score 290; DB 2; Length 459;		
Best Local Similarity 33.5%; Pred. No. 1e-14;		A; Best Local Similarity 33.5%; Pred. No. 1e-14;
Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;		A; Cross-references: UNIPROT:P27512; GB:MB3312; NID:91553058
Qy 8 PYASE-NOTCRDQEKEYEPQRHICCSRCRCPGTYVSAKCSRIRDTCATCAENSYNEHWN 66		A; Note: sequence extracted from NCBI backbone (NCBInr:75207)
Db 16 PYKEPPGTECQLISQ-EYDRKAQMCCAKCPGQYVKHEFCNKTSDTVCAADCASMYTQWN 74		A; Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
Qy 67 YLTICQLCRPDPVMGLEBIAPTSKRKTQCRKQCPGMFCAAVALCPTCBLUSDCPPETE 121		R; Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, B.A.; Howard, M.; Cockayne, R; Torres, R.M.; Clark, B.A.
Db 75 QFPITCLSSSCTDQV---ETRACTKQNRVCAEAGRYCALTKHGSRCMRSLSKC 130		J. Immunol. 148, 620-626, 1992
Qy 122 PPGTEAELKDEVGKGNNNCVPCKAGHFTQNTSSSARCPHTRCENQIIVRAAPGTAQSDT 181		A; Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40 gene.
Db 131 GPSP-GVASSRAPNGNVTLCKACAPGTFSTDTDVPHRCS---ILATPGNASTDA 185		A; Reference number: A46515; PMID:1370315
Qy 182 TCKNPLBLPPMNS 195		A; Accession: A46476
Db 186 VC---ABESPTL 195		A; Status: preliminary
<b>RESULT 5</b>		
A60771	B-cell activation protein CD40 precursor - human	A; Molecule type: mRNA A; Residues: 1-305 <TOR>
N; Alternative names: B-cell surface antigen Bp50		A; Cross-references: UNIPROT:P27512; GB:MB3312; NID:91553058; PMID:91553059; GB:MB4126; I
C; Species: Homo sapiens (man)		A; Note: sequence extracted from NCBI backbone (NCBInr:120357)
C; Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004		A; Comment: For an alternative splice form, see PIR:A46515.
R; Stamenkovic, I.; Clark, B.A.; Seed, B.		C; Comment: For an alternative splice form, see PIR:A46476.
EMBO J. 8, 1403-1410, 1989		C; Superfamily: CD27 antigen; NGF receptor repeat homology
A; Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor		C; Keywords: alternative splicing; transmembrane protein
A; Reference number: S04460; PMID:2475341		F:105-144/Domain: NGF receptor repeat homology <NGF>
A; Accession: S04460		
A; Molecule type: mRNA		
A; Residues: 1-277 <SPN>		Query Match 21-5*: Score 243.5; DB 2; Length 305;
A; Cross-references: UNIPROT:P25342; EMBL:X60592; NID:929850; PID:CAA3045.1; PID:929851		Best Local Similarity 31.0%; Pred. No. 2.3e-11;
R; Braess-Andersen, S.; Paulie, S.; Koho, H.; Aspenstroem, P.; Perlmann, P.		Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;
J. Immunol. 142, 562-567, 1989		
A; Biochemical characteristics and partial amino acid sequence of the receptor-like		Qy 15 TCRDQEKEYEPQRHICCSRCRCPGTYVSAKCSRIRDTCATCAENSYNEHNTLCOLC 74
A; Accession: A60771		Db 25 TCSD--QYLNHDQ--CDLCOGPGRSLTSHCTALEKTQCHPCDSIGFBFAQMNREIRCHQH 80
A; Molecule type: protein		
A; Residues: 21-50  		

Qy	75 RPPCDPVMSGLEETIAPCTSRRKTCRQPMFCAAWALECTHCELLSDCPG-----TEAEL 129	Query Match Score 19.6%; DB 2; Length 271;
Db	81 RHEBPNQLRVRKEGTIARSDTIVTCRKEQHCT---SKDVEAQAHQTPCIPGREGMENATE 138	Best Local Similarity 32.1%; Pred. No. 7.8e-10; Matches 53; Conservative 17; Mismatches 68; Indels 6 27; Gaps 5;
Qy	130 KDEVGKGNHVCYPCCKAGHFFQNTSSPSARCPHTRCENQGLIVEAAPGTAQSDFTC 183	Qy 21 KEYYEPOHRICCSRPGTYVSAKCSRIRDTCVATCAENSYNEHHNNYLTCQLCRCDPV 80
Db	139 TDTV-----CHCPCVGFPSNQSSLERKCFPWTSCEDNLLEVQKGTSQTNVIC 186	Db 28 KHTYPSGHK---CCRECPGFGHGVSRCDHTRDTCVCPCEPGFNEAVAYNDT---CKQCQCNHR 85
<b>RESULT 7</b>		
death receptor-6 - chicken		
C;Species:	Gallus gallus (chicken)	Qy 81 MGLEIAPCTSRRKTCRQCPGMFCAAWALECTHCELLSDCPGTAELKDEVGKGNHNC 140
C;Date:	09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004	Db 86 SGSELQNCTPTEDTVCQCR-----PGQPR-QDSSSHKLGVDC 122
C;Accession:	JC7705	Qy 141 VPCKAGHFONTSSPSARCPHTRCENQGLIVEAAPGTAQSDFTC 185
R;Bridgeman, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.	Db 123 VPCPPGHPSPSNSQNA--CKPWNCTLSGKQIRHAPSNSLDTCVED 165	
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001		
A;Title:	Conservation of death receptor-6 in avian and piscine vertebrates.	
A;Reference number:	JC7705; PMID:21308433; PMID:11414698	
A;Accession:	JC7705	RESULT 9
A;Molecule type:	mRNA	148700
A;Residues:	1-651  	gene ox40 protein - mouse
A;Cross-references:	UNIPROT:Q98SM6; GB:AF49908	N;Alternative names: OX40 antigen
C;Comment:	This receptor, a member of the tumor necrosis factor receptor family, belongs to a cell death and/or survival signaling cascade.	C;Species: Mus musculus (house mouse)
C;Generics:		C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
A;Gene:	dr-6	C;Accession: I48700; 148334; S34377
C;Superfamily:	tumor necrosis factor receptor type 1 (TNFR1) ; NGF receptor repeat homolog	R;Calderhead, D.M.; Buhmann, J.B.; van den Bertwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993
C;Keywords:	ovary	A;Title: Cloning of mouse Ox40, a T cell activation marker that may mediate T-B cell int
F1-21/Domain:	signal sequence #status predicted <SIG>	A;Reference number: I48700; 148700; PMID:9044750; PMID:8228223
F52-196/Domain:	extracellular cysteine-rich, ligand-binding #status predicted <TMM>	A;Status: translated from GB/EMBL/DDJB
F410-475/Domain:	transmembrane #status predicted <TMM>	A;Cross-references: UNIPROT:PA74741; EMBL:Z221674; NID:931287; PID:931281
P551-651/Region:	death domain #status predicted <DBD>	R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
C;Region: conserved cycloplasmic #status predicted		
Query Match Score 20.0%; Best Local Similarity 28.8%; Pred. No. 7.8e-10; Matches 49; Conservative 26; Mismatches 62; Indels 33; Gaps 6;	Qy 130 ICSSRCRPGTYVSAKCSRIRDTCVATCAENSYNEHHNNYLTCQLCRCDPV 88	Qy 21 KEYYEPOHRICCSRPGTYVSAKCSRIRDTCVATCAENSYNEHHNNYLTCQLCRCDPV 80
Db	50 LTKDKCPGTYVSKHCKTKSTLRECSPCPGTFPKHENGIERCHPKCKPE--LPMTKTH 107	Db 29 KHTYPSGHK---CCRECPGFGHGVSRCDHTRDTCVCPCEPGFNEAVAYNDT---CKQCQCNHR 86
Qy	89 CTSRKRTQCRQGMF-----CRAWALECTHCELLSDCPG-----PGTEAELKDEVKG 136	Qy 81 MGLEIAPCTSRRKTCRQCPGMFCAAWALECTHCELLSDCPGTAELKDEVGKGNHNC 140
Db	108 CTALTDRCITCLSGTFQNDTCVPTY-----CPVGMGVRKGKTE----- 149	Db 87 SGSELQNCTPTEDTVCQCR-----PGQPR-QDSSSHKLGVDC 123
Qy	137 NNHCVPCKAGHFONTSSPSARCPHTRCENQGLIVEAAPGTAQSDFTC 186	Qy 141 VPCKAGHFONTSSP--SARCOPHTRCENQGLIVEAAPGTAQSDFTC 185
Db	150 DVRCKPCLRGTFSDVPSVMKCKTYYTFQGRNMVVVKPGTKESDNVCKSP 199	Db 124 VPCPPGHPF---SPGNQQACKWPNTLSGKOTRHPASDSLDAVCE 166
<b>RESULT 8</b>		
S12783	OX40 antigen precursor - rat	RESULT 10
N;Alternative names:	nerve growth factor receptor homolog	GHOUT1
C;Species:	Rattus norvegicus (Norway rat)	tumor necrosis factor receptor 1 precursor [validated] - human
C;Date:	30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004	N;Alternative names: P55 tumor necrosis factor receptor type 1
R;Mallett, S.; Barclay, A.N.		N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
EMBO J. 9, 1063-1068, 1990		C;Species: Homo sapiens (man)
A;Title:	Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes	C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
A;Reference number:	S12783; MUI:9021461; PMID:217591	C;Accession: A38208; A34599; A34900; A36555; C36555; A3828L; S12057; JT0758; A60231; A381R; Fuchs, P.; Strehl, S.; Dworzak, M.; Himmller, A.; Ambros, P.F.
A;Accession:	S12783	
A;Molecule type:	mRNA	
A;Residues:	1-271	
A;Cross-references:	UNIPROT:PI5725; EMBL:X17037; NID:957830; PID:CAA34897.1; PID:957831	
C;Superfamily:	CD27 antigen; NGF receptor repeat homolog	
C;Keywords:	growth factor receptor; transmembrane protein	
F1-19/Domain:	signal sequence #status predicted <SIG>	
F20-27/Domain:	OX40 antigen #status predicted <NAT>	
F21-235/Domain:	transmembrane #status predicted <TMM>	

Genomics 13, 219-224, 1992  
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to chromosome 13. Reference number: A33208; MUID:92250049; PMID:1313717

A;Accession: A38208  
A;Molecule type: DNA  
A;Residues: 1-455 <FUC>  
A;Cross-references: UNIPROT:P19438; GB:M75865; GB:M75866; PIDN:9339748; PIDN:2701161; Lantz, M.; Nilsson, E.; Peetre, C.; Thyssell, H.; Grubb, A.; Adolf, G.  
R;Loetscher, H.; Pan, Y.C.E.; Lahn, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau Cell 61, 351-359, 1990  
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor. Reference number: A34899; MUID:90235284; PMID:2158862  
A;Accession: A34899  
A;Molecule type: mRNA  
A;Residues: 1-455 <LOB>  
A;Cross-references: GB:MS8286; GB:MS3480; PIDN:AAA36753.1; PID:9339754  
A;Experimental source: placenta  
A;Note: part of this sequence, including the amino end of the mature protein, was confirmed by Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatangala, T. Cell 61, 361-370, 1990  
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor. Reference number: A34900; MUID:90235285; PMID:2158863  
A;Accession: A34900  
A;Molecule type: mRNA  
A;Residues: 1-455 <SCH>  
A;Cross-references: GB:M33294; PIDN:AAA03210.1; PID:9339745  
R;Himmeler, A.; Maurer-Pogoy, I.; Kroenke, M.; Scheurich, P.; Peitschmaier, K.; Lantz, M.; DNA Cell Biol. 9, 705-715, 1990  
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor receptors. Reference number: A36555; MUID:91090841; PMID:1702293  
A;Accession: A36555  
A;Molecule type: mRNA  
A;Residues: 1-455 (HIM)>  
A;Cross-references: GB:M63121; PIDN:AAA36754.1; PID:9339756  
A;Accession: C36555  
A;Molecule type: Protein  
A;Residues: 30-3841-51,'X',55-79,'XX',82-94,'NR','XX',100-104;107-128;162-167,'X',169-210  
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble protein. Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990  
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of receptor. Reference number: A38281; MUID:91017509; PMID:2170974  
A;Accession: A38281  
A;Molecule type: mRNA  
A;Residues: 1-455 <NG2>  
A;Cross-references: GB:M37764  
A;Accession: S12057  
A;Molecule type: mRNA  
A;Residues: 1-455 <NOB>  
A;Cross-references: ENBL:X55313; PIDN:CAA39021.1; PID:937224  
A;Reference number: J70758; MUID:94085779; PMID:8262379  
A;Accession: J70758  
A;Molecule type: DNA  
A;Residues: 1-13 <KEM>  
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
Bur. J. Immunol. 20, 1167-1174, 1990  
A;Title: Tumor necrosis factor inhibitor purification, NH-2-terminal amino acid sequence. Reference number: A60231; MUID:90292116; PMID:2113477  
A;Accession: A60231  
A;Molecule type: protein  
A;Residues: 41-43,'X',45-53,'X',55-57 <SEG>  
R;Gatangala, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor)

tients. Reference number: A38258; MUID:91062364; PMID:2174164  
A;Accession: A38258  
A;Molecule type: Protein  
A;Residues: 41-60 <GAT>  
A;Experimental source: cancer patient serum  
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyssell, H.; Grubb, A.; Adolf, G.  
Eur. J. Haematol. 42, 270-275, 1989  
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from A;Reference number: A60594; MUID:89171156; PMID:2924890  
A;Accession: A60594  
A;Molecule type: protein  
A;Residues: 41-43,'X',45-53,'V',55-57,'XR',60 <OLS>  
A;Experimental source: renal failure patient urine  
R;Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A;Reference number: A35010; MUID:90110215; PMID:2153136  
A;Accession: A35010  
A;Molecule type: protein  
A;Residues: 41-45 <ENG>  
A;Experimental source: normal urine  
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
Biosci. Biotechnol. Biochem. 58, 226-228, 1994  
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified A;Reference number: JC2404; MUID:95128033; PMID:7765720  
A;Accession: JC2404  
A;Molecule type: protein  
A;Residues: 41-51,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>  
A;Experimental source: urine  
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and C;Genetics:  
A;Gene: GDB:TNFRI  
A;Cross-references: GDB:125913; OMIM:191190  
A;Map position: 12p13.2-12p13.2  
A;Introns: 13/3; 65/1; 108/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homologous; duplication; glycoprotein; receptor; transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-55/Domain: tumor necrosis factor receptor #status predicted <MAT>  
P;30-211/Domain: extracellular #status predicted <EXT>  
F;41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status predicted <INT>  
P;44-82/Domain: NGF receptor repeat homology <NG1>  
P;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-196/Domain: NGF receptor repeat homology <NG4>  
P;212-234/Domain: transmembrane #status predicted <MEM>  
P;235-455/Domain: intracellular #status predicted <INT>  
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted <EXT>

Query Match 18.6%; Score 210.5; DB 1; Length 455;  
Best Local Similarity 32.6%; Pred. No. 9.3e-09;  
Matches 61; Conservative 19; Mismatches 84; Indels 23; Gaps 9;

Qy 18 DOBK-----EYBPOHR-ICCSRCRCPGPTVYSAK-SRIRDTCATCAENSNTWNY 67  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
36 DREKRDSEVCPQSKRCKHKGTYLYNDPGPGDFTDCRECESSSFASBNH 95

Qy 68 LTCIQLQCRPCDPVMGLEBIAPCTSRTKTOCQGMFCAAVA--LBCTHCBLLSDCPPG 124  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
96 LRHCLSCSKRKEMGQVEISSTCVDTCGCRKNQYRHYNSENLFQCFCNSL--CLNG 152

Qy 125 TEAEIQLDVBGRKNNHCVPKRAGHF--ONTSSPSARCOPHTRGENGH--VEAAPGTAQSD 180  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
153 TVHLSQCE-KONTVCT-CHAGFFLRLNECTCSNCKSSELECTKLCPQIENVKGTEDSG 209

Qy 181 TTCKNPPL 187  
Db :|||:|||:  
210 TTVLPL 216

RESULT 11  
T28623

Hypothetical protein G2R - variola major virus

C;Species: Variola major virus  
 C;Accession: T28633  
 C;Sequence\_revision: 22-Oct-1999 #text\_change 09-Jul-2004  
 R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin, Natura 366, 78-751, 1993  
 A;Title: Potential virulence determinants in terminal regions of variola smallpox virus  
 A;Reference number: Z20488; MUIID:94088747; PMID:8264798  
 A;Accession: T28633  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-349 <MAS>  
 A;Cross-references: UNIPROT:P34015; EMBL:122579; PIDN:9623595; PID:9449137.1; PID:g4391  
 A;Experimental source: strain Bangladesh 1975  
 A;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology  
 Query Match 18.5%; Score 210; DB 2; Length 349;  
 Best Local Similarity 29.0%; Pred. No. 8.3e-09;  
 Matches 45; Conservative 20; Mismatches 80; Indels 10; Gaps 5;  
 Result 12

Qy 8 PYASENQCRDQKEYYFQHQRICCSRGPPGTVUSAKCSRBDTVCATCAENSYNHWY 67  
 Db 23 PYTPNGKCKDTBK ---RHNLCLSCSPGTYASRLCDSKTNTOCPCGSCTETSRNNH 78  
 Qy 68 LTICQLCR-PCDPVMGLEBIAPCTSKRKTQCRQGMFC-AWAALECTHCCELLSDCPPGT 125  
 Db 79 LPACLSNGRN -SNOVETRSNCNTTHNRICECSPGTYCLLKSSGCKACTQSOKC-GI 134  
 Qy 126 EAELKDEVGKGNNHCVPKAGHFQNTSSPSARCP 160  
 Db 135 GYGVSIGHTSVGDVICSPCGFTYSHTVSSADKEP 169

Result 13

Qy 8 PYASENQCRDQKEYYFQHQRICCSRGPPGTVUSAKCSRBDTVCATCAENSYNHWY 67  
 Db 23 PYTPNGKCKDTBK ---RHNLCLSCSPGTYASRLCDSKTNTOCPCGSCTETSRNNH 78  
 Qy 68 LTICQLCR-PCDPVMGLEBIAPCTSKRKTQCRQGMFC-AWAALECTHCCELLSDCPPGT 125  
 Db 79 LPACLSNGRN -SNOVETRSNCNTTHNRICECSPGTYCLLKSSGCKACTQSOKC-GI 134  
 Qy 126 EAELKDEVGKGNNHCVPKAGHFQNTSSPSARCP 160  
 Db 135 GYGVSIGHTSVGDVICSPCGFTYSHTVSSADKEP 170

Result 14

Qy 8 PYASENOTCRDQEKEYYFQHQRICCSRGPPGTVUSAKCSRBDTVCATCAENSYNHWY 67  
 Db 24 PYTPNGKCKDTBK ---RHNLCLSCSPGTYASRLCDSKTNTOCPCGSCTETSRNNH 79  
 Qy 68 LTICQLCR-PCDPVMGLEBIAPCTSKRKTQCRQGMFC-AWAALECTHCCELLSDCPPGT 125  
 Db 80 LPACLSNGRN -SNOVETRSNCNTTHNRICECSPGTYCLLKSSGCKACTQSOKC-GI 135  
 Qy 126 EAELKDEVGKGNNHCVPKAGHFQNTSSPSARCP 160  
 Db 136 GYGVSIGHTSVGDVICSPCGFTYSHTVSSADKEP 170

A;Cross-references: UNIPROT:P34015; GB:Y16780; NID:9583055; PIDN:CA854798.1; PID:g58307  
 A;Cross-references: UNIPROT:P34015; GB:Y16780; NID:9583055; PIDN:CA854798.1; PID:g58307  
 C;Sequence\_revision: 24-Nov-1999 #text\_change 09-Jul-2004  
 C;Accession: D72175  
 R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998  
 A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor  
 A;Reference number: A72150  
 A;Accession: D72175  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-249 <SHC>  
 A;Cross-references: UNIPROT:P34015; GB:Y16780; NID:9583055; PIDN:CA854798.1; PID:g58307  
 A;Experimental source: Strain Garcia-1966  
 C;Genetic:  
 A;Gene: G2R  
 C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology  
 Query Match 18.3%; Score 207; DB 2; Length 349;  
 Best Local Similarity 29.0%; Pred. No. 1.4e-08;  
 Matches 45; Conservative 19; Mismatches 81; Indels 10; Gaps 5;  
 Result 15

Qy 8 PYASENOTCRDQEKEYYFQHQRICCSRGPPGTVUSAKCSRBDTVCATCAENSYNHWY 67  
 Db 24 PYTPNGKCKDTBK ---RHNLCLSCSPGTYASRLCDSKTNTOCPCGSCTETSRNNH 79  
 Qy 68 LTICQLCR-PCDPVMGLEBIAPCTSKRKTQCRQGMFC-AWAALECTHCCELLSDCPPGT 125  
 Db 80 LPACLSNGRN -SNOVETRSNCNTTHNRICECSPGTYCLLKSSGCKACTQSOKC-GI 135  
 Qy 126 EAELKDEVGKGNNHCVPKAGHFQNTSSPSARCP 160  
 Db 136 GYGVSIGHTSVGDVICSPCGFTYSHTVSSADKEP 170

A;Cross-references: UNIPROT:P34015; GB:Y16780; NID:9583055; PIDN:CA854798.1; PID:g58307  
 A;Cross-references: UNIPROT:P34015; GB:Y16780; NID:9583055; PIDN:CA854798.1; PID:g58307  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
 C;Accession: JC4302; PC4093  
 R;Sutur, B.; Pauli, U.  
 Gene 163; 263-266, 1995  
 A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
 A;Reference number: 96011645; PMID:7590278  
 A;Accession: JC4302  
 A;Molecule type: mRNA  
 A;Residues: 1-161 <SDT>  
 A;Cross-references: UNIPROT:P30555; GB:U19934; NID:g1141752; PMID:911417  
 A;Accession: PC4093  
 A;Molecule type: protein  
 A;Residues: 1-7 <SU2>

A;Gene: G4R  
 A;Cross-references: UNIPROT:P34015; GB:Y16780; NID:9583055; PIDN:CA854798.1; PID:g58307  
 C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology <NGF>  
 F;68-109/Domain: NGF receptor repeat homology <NG2>

A:Experimental source: kidney cell line 15

C:Genetics:

A:Gene: tnf

C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog

C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor

P:-29/Domain: signal sequence #status predicted &lt;SIG&gt;

P:30-46/Product: tumor necrosis factor receptor p55 #status predicted &lt;MAT&gt;

P:44-194/Domain: extracellular cysteine rich #status predicted &lt;EXT&gt;

P:44-82/Domain: NGF receptor repeat homology &lt;NGF&gt;

P:84-126/Domain: NGF receptor repeat homology &lt;NGF&gt;

P:211-231/Domain: transmembrane #status predicted &lt;TM&gt;

P:361-447/Domain: signal transduction #status predicted &lt;SIT&gt;

P:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.2%; Score 206; DB 2; Length 461;

Best Local Similarity 29.4%; Pred. No. 2.1e-08; Matches 57; Conservative 22; Mismatches 77; Indels 38; Gaps 9;

Db .

Qy 18 DQEK-----EYEPDHR-ICCSRCPPTVYSAKC-SRIRDTCATCAENSYEHNNY 67

Db 36 DREKRESLCPGKYSHPQRNSICCTKCHRGTYLHNDCLGPGLDNDCRBDNGPFPTASRNH 95

Qy 68 LTICOLCRPCDPVNGLEIAAPCTSKRKTKTQCRCPGMFCZAWA---LETHTCBLLSDCPG 124

Db 96 LTOCLCSKCSRSENSQSVLISPCTVDRDTVCGCKKNQYKWSSTLFFQCLNCSL--CFNG 152

Qy 125 TE---ABLKDEVERGNHNCVCPKAGHFONTSSPSARCOPHTRCENQSLIVEAPGTAQ-- 178

Db 153 TVQLPCLERQDTI-----CNCHSGFPLR----DKECVSYCNICKNAOCKNLCPATSETR 201

Qy 179 -----SDTICKNPL 187

Db 202 NDFDFTGTVLLPL 215

## RESULT 15

I37552

OK40 homolog - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004

C:Accession: I37552

R:Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Bitelbach, F.; Hummel, M.; Fonat

R:J. Immunol. 24, 677-683, 1994

A&gt;Title: The human OK40 homolog: cDNA structure, expression and chromosomal assignment

A:Reference number: I37552; MUID:94170844; PMID:7510240

A:Accession: I37552

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-277 &lt;RES&gt;

A:Cross-references: UNIPROT:P43489; EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:g4729

C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 17.7%; Score 201; DB 2; Length 277;

Best Local Similarity 28.3%; Pred. No. 3.3e-08; Matches 49; Conservative 21; Mismatches 73; Indels 30; Gaps 5;

Db .

Qy 26 PQHRCICSRCPPTVYSAKCCSRIRDTCATCAENSYEHNNYLTICQCRCDPVMGLIE 85

Db 37 PSNDRCCHECRPGNGMVSRCRSQNTVCRPCGPGPYNDVSSKP-CFKETWCLRLSSSER 95

Qy 86 IAPCTSKRKTKCOPGMFCAAWALECBTCELLSDCPPGEALKDEVKGNNHHCVPCKA 145

Db 96 KQLCTATQDTVCRCAG-----TQPUDSYKGV-----CAUCPP 130

Qy 146 GHFQNTSSPSARCOPHTRCENQSIVEAAPGTAQOSDITC-KNPLEPLPEMSG 196

Db 131 GHF--SPGDNQACKPWTNCTLACKHTLQDPAASNDSAICEDRDPATQQETQG 181

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Scoring table:	BLOSUM62				
Gapopen:	10.0	Gapext: 0.5			
Searched:	1612378 seqs,	512079187 residues			
Total number of hits satisfying chosen parameters:	1612378				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0%				
	Maximum Match 100%				
	Listing first 45 summaries				
Database :	UniProt_03_*	*			
	1: <u>Uniprot_sprot</u>	*			
	2: <u>Uniprot_trembl</u>	*			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	435	1 TNR3_HUMAN	P26941 homo sapien
2	771	68.0	415	1 TNR3_MOUSE	P50284 mus musculus
3	309.5	27.3	483	2 Q800k7	Q800k7 paralichthys
4	290.5	26.9	461	1 TR1B_HUMAN	P20333 human tumor necrosis factor receptor beta
5	295.5	26.1	278	2 Q8sq74	Q8sq74 sus scrofa
6	295	26.0	474	1 TR1B_MOUSE	P25119 mus musculus
7	291.5	25.7	433	2 Q91zmg	Q91zmg6 rat
8	291.5	25.7	461	2 Q6vau8	Q6vau8 rat
9	291.5	25.7	474	1 TR1B_RAT	Q8bwY6 rat
10	280	25.6	459	2 Q62327	Q62327 mouse
11	285.5	25.2	300	1 TR6B_HUMAN	Q5j407 homo sapiens
12	284.5	25.1	274	2 Q7yrus	Q7yr05 canis familiaris
13	283	25.0	625	1 TR1I_MOUSE	Q33305 mus musculus
14	278	24.5	223	2 Q8t1f5	Q8yqk5 homo sapiens
15	278	24.5	277	1 TNR5_HUMAN	P29442 homo sapiens
16	277	24.4	616	1 TR1I_HUMAN	Q9y6q6 homo sapiens
17	266.5	23.5	387	2 Q6GLn3	Q6GLn3 xenopus laevis
18	265.5	23.4	277	2 Q8wmq2	Q8wmq2 ovis aries
19	258	22.8	275	2 Q80wm9	Q80wm9 mus musculus
20	258	22.8	276	2 Q71f55	Q71f55 mus musculus
21	253	22.3	462	2 Q80f55	Q80f55 mus musculus
22	251.5	22.2	269	1 TNR5_BOVIN	Q28203 bos taurus
23	246.5	21.8	401	2 Q6P1T2	Q5P1T2 mus musculus
24	243.5	21.5	289	1 TNR5_MOUSE	P27512 mus musculus
25	242.5	21.5	283	2 Q8K2X6	Q8K2X6 mus musculus
26	242.5	21.4	283	2 Q9X5Z8	Q9X5Z8 cercopithecus
27	242.5	21.4	401	1 T11B_MOUSE	Q08712 mus musculus
28	239	21.2	186	2 Q7235	Q7235 cowpox virus
29	239.5	21.1	401	1 T11B_HUMAN	Q00300 homo sapiens
30	238.5	21.1	318	2 Q7tRH3	Q7tRH3 oncophryncus
31	238	21.0	302	2 Q9PUS0	Q9PUS0 salvinius

## ALIGNMENTS

RESULT 1	
TNR3_HUMAN	STANDARD;
ID P36941;	PRT; 435 AA.
AC F36941;	
DT 01-JUN-1994 (Rel. 29, Created)	
DT 01-JUN-1994 (Rel. 29, Last sequence update)	
DT 05-JUL-2004 (Rel. 44, Last annotation update)	
DE Tumor necrosis factor receptor superfamily member 3 precursor	
DB (Lymphotxin-alpha receptor) (Tumor necrosis factor receptor superfamily member 3 precursor)	
DB (Lymphotxin-beta receptor) (Tumor necrosis factor receptor superfamily member 3 precursor)	
GN Name=TNFRBR; Synonyms=TNFRCR, TNFRSF3;	
OS Homo sapiens (Human)	
OC Mammalia; Buteraria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi; Hominidae; Homininae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCES FROM N.A.	
RC TISSUE=Liver;	
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.,	
RA "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid.";	
RL Genomics 16:214-218(1993). <sup>[2]</sup>	
RN [2]	
RP SEQUENCES FROM N.A.	
RC TISSUE=Lung;	
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA Strasburg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Zeeberg B., Buetow K.H., Schaefer C.P., Altenschul S.F., Bhat N.K., Buetow K.H., Buetow K.H., Bhat N.K., Buetow K.H., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Ketteman M., Madan A., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E., Scheiner A., Schein J.E., Jones S.J.M., Marrs M.A./	
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|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| [4] | RN CHARACTERIZATION; PubMed=10207006; DOI=10.1074/jbc.274.17.11868;                                                                                           | RN RP MEDLINE=9223511; PubMed=10207006; DOI=10.1074/jbc.274.17.11868;                                                                                                              |
| RX  | RW Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;                                                                                                              | RX RA "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell death in HeLa cells." RT ;                                                                            |
| RA  | RW Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;                                                                                                     | RT RT "The lymphotoxin-beta receptor is necessary and sufficient for LIGHT-mediated apoptosis of tumor cells";                                                                     |
| RA  | RW Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A., Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;                              | RT J. Biol. Chem. 274:11868-11873 (1999). [5]                                                                                                                                      |
| RN  | RN MEDLINE=20261554; PubMed=10799510; DOI=10.1074/jbc.275.19.14307;                                                                                           | RN RP MEDLINE=20261554; PubMed=10799510; DOI=10.1074/jbc.275.19.14307;                                                                                                             |
| RX  | RW Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A., Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;                              | RT RT "The lymphotoxin-beta receptor is necessary and sufficient for LIGHT-mediated apoptosis of tumor cells";                                                                     |
| RA  | RW Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;                                                                                                     | RT J. Biol. Chem. 275:14307-14315 (2000). [6]                                                                                                                                      |
| RN  | RN INTERACTION WITH TRAF3.                                                                                                                                    | RN RP INTERACTION WITH TRAF3.                                                                                                                                                      |
| RX  | RW MEDLINE=92289293; PubMed=8663299; DOI=10.1074/jbc.271.25.14561;                                                                                            | RT RX MEDLINE=92289293; PubMed=8663299; DOI=10.1074/jbc.271.25.14561;                                                                                                              |
| RA  | RW Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F., Yagita H., Okumura K.;                                                                      | RT RA "TRAF5, an activator of NF-kappaB and putative signal transducer for the lymphotoxin-beta receptor";                                                                         |
| RA  | RW Yagita H., Okumura K.;                                                                                                                                     | RT Am. J. Pathol. 152:1549-1561 (1998). [9]                                                                                                                                        |
| RN  | RN INTERACTION WITH TRAF4.                                                                                                                                    | RN RP INTERACTION WITH TRAF4.                                                                                                                                                      |
| RX  | RW MEDLINE=96289299; PubMed=9626059;                                                                                                                          | RT RX MEDLINE=96289299; PubMed=9626059;                                                                                                                                            |
| RA  | RW Krajevska M., Krajevska S., Zapata J.M., VanArsdale T., Gascayne R.D., Berem K., McFadden D., Shabalk A., Hugh J., Reynolds A., Cleverger C.V., Reed J.C.; | RT RA "Cloning and characterization of a cDNA encoding the human homolog of TRAF4 expression in epithelial progenitor cells. Analysis in normal adult, fetal, and tumor tissues."; |
| RA  | RW Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M., Otsuka M., Yamamoto T., Inoue J.-I.;                                                   | RT RT Gene 207:1335-140 (1998).                                                                                                                                                    |
| RN  | RN INTERACTION WITH TRAF5.                                                                                                                                    | RN RP INTERACTION WITH TRAF5.                                                                                                                                                      |
| RX  | RW MEDLINE=9511754; PubMed=9511754; DOI=10.1016/S0378-1119(97)00616-1;                                                                                        | RT RX MEDLINE=9511754; PubMed=9511754; DOI=10.1016/S0378-1119(97)00616-1;                                                                                                          |
| RA  | RW Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M., Otsuka M., Yamamoto T., Inoue J.-I.;                                                   | RT RA "Cloning and characterization of a cDNA encoding the human homolog of tumor necrosis factor receptor-associated factor 5 (TRAF5)."; RT Gene 207:1335-140 (1998).             |
| RL  | RW -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing LTA and LTb, and for TNFSF4/Light. Promotes apoptosis via TRAF3 and TRAF5.            | RT -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing LTA and LTb, and for TNFSF4/Light. Promotes apoptosis via TRAF3 and TRAF5.                                 |
| RL  | RW -1- SUBUNIT: Self-associates Associates with TRAF3, TRAF4 and TRAF5.                                                                                       | RT -1- SUBUNIT: Self-associates Associates with TRAF3, TRAF4 and TRAF5.                                                                                                            |
| RL  | RW -1- SIMILARITY: Contains 4 TNFR-Cys repeats.                                                                                                               | RT -1- SIMILARITY: Contains 4 TNFR-Cys repeats.                                                                                                                                    |
| CC  | CC                                                                                                                                                            | CC                                                                                                                                                                                 |
| DR  | DR MIM: 6005979; -.                                                                                                                                           | CC DR MIM: 6005979; -.                                                                                                                                                             |
| DR  | DR GO: GO:0055151; F:protein binding; IPI.                                                                                                                    | CC DR GO: GO:0055151; F:protein binding; IPI.                                                                                                                                      |
| DR  | DR GO: GO:0048711; F:signal transducer activity; IEP.                                                                                                         | CC DR GO: GO:0048711; F:signal transducer activity; IEP.                                                                                                                           |
| DR  | DR GO: GO:0033123; P:positive regulation of I-kappaB kinase/NF-k. . . ; IEP.                                                                                  | CC DR GO: GO:0033123; P:positive regulation of I-kappaB kinase/NF-k. . . ; IEP.                                                                                                    |
| DR  | DR HSSP: Q9256; 1JMA.                                                                                                                                         | CC DR HSSP: Q9256; 1JMA.                                                                                                                                                           |
| DR  | DR Gene; HGNC: 6718; LTPR.                                                                                                                                    | CC DR Gene; HGNC: 6718; LTPR.                                                                                                                                                      |
| DR  | DR H-InvDB; HIX0010362; -.                                                                                                                                    | CC DR H-InvDB; HIX0010362; -.                                                                                                                                                      |
| DR  | DR MIM: 6005979; -.                                                                                                                                           | CC DR MIM: 6005979; -.                                                                                                                                                             |
| DR  | DR GO: GO:0055151; F:protein binding; IPI.                                                                                                                    | CC DR GO: GO:0055151; F:protein binding; IPI.                                                                                                                                      |
| DR  | DR GO: GO:0048711; F:signal transducer activity; IEP.                                                                                                         | CC DR GO: GO:0048711; F:signal transducer activity; IEP.                                                                                                                           |
| DR  | DR GO: GO:0033123; P:positive regulation of I-kappaB kinase/NF-k. . . ; IEP.                                                                                  | CC DR GO: GO:0033123; P:positive regulation of I-kappaB kinase/NF-k. . . ; IEP.                                                                                                    |
| DR  | DR GO: GO:0011651; P:signal transduction; IAS.                                                                                                                | CC DR GO: GO:0011651; P:signal transduction; IAS.                                                                                                                                  |
| DR  | DR InterPro: IPR008063; Fas receptor.                                                                                                                         | CC DR InterPro: IPR001368; TNFR_C6.                                                                                                                                                |
| DR  | DR InterPro: IPR002020; TNFR_C6.                                                                                                                              | CC DR InterPro: IPR002020; TNFR_C6.                                                                                                                                                |
| DR  | DR PRINTS: PR01680; FARRECEPTOR.                                                                                                                              | CC DR PRINTS: PR01680; FARRECEPTOR.                                                                                                                                                |
| DR  | DR SMART: SM00208; FARRECEPTOR.                                                                                                                               | CC DR SMART: SM00208; FARRECEPTOR.                                                                                                                                                 |
| DR  | DR PROSITE: PS00652; TNFR_NGFR_1.                                                                                                                             | CC DR PROSITE: PS00652; TNFR_NGFR_1.                                                                                                                                               |
| DR  | DR PROSITE: PS00050; TNFR_NGFR_2.                                                                                                                             | CC DR PROSITE: PS00050; TNFR_NGFR_2.                                                                                                                                               |
| DR  | DR MEDLINE=9616385; PubMed=8586432;                                                                                                                           | CC DR MEDLINE=9616385; PubMed=8586432;                                                                                                                                             |
| RA  | RA Nakamura T.; Tashiro K.; Nazarea M.; Nakano T.; Sasayama S.; Honjo T.;                                                                                     | CC RA Nakamura T.; Tashiro K.; Nazarea M.; Nakano T.; Sasayama S.; Honjo T.;                                                                                                       |

"The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping.",  
Genomics 30:312-319 (1995).  
[3]

INTERACTION WITH TRAF5.  
STRAIN:BALB/c;  
MEDLINE=96278943; Published=8653299; DOI=10.1074/jbc.271.25.14661;  
Nagano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,  
Yagita H., Okumura K.;  
"TRAF5, an activator of NF-kappaB and putative signal transducer for the lymphotoxin-beta receptor.",  
J. Biol. Chem. 271:14661-14664 (1996).  
-!- FUNCTION: Receptor for the heterotrimeric lymphokines containing LT $\alpha$  and LT $\beta$ , and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3 and TRAF5. May play a role in the development of lymphoid organs  
(By similarity).  
-!- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.  
Associates with TRAF3 and TRAF4 (By similarity).  
-!- SUBCELLULAR LOCATION: Type I membrane protein.  
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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EMBL; U29173; AAA68964.1;	-.
EMBL; L38423; AAB00846.1;	-.
EMBL; U30798; AAQ81334.1;	-.
HSSP; Q14763; 1DQ3	
MGD; MGI:104875; Ltbr.	
InterPro; IPR01368; TNFR_c6.	
Pfam; PF00020; TNFR_c6;	3.
SMART; SM00208; TNFR_3.	
PROSITE; PS00052; TNFR_NGFR_1;	2.
PROSITE; PS00050; TNFR_NGFR_2;	3.
APOPROSIS; Glycoprotein_Receptor;	
SIGNAL; 1 30	Repeat; Signal; Transmembrane.
CHAIN 31 415	Potential.
DOMAIN DOMAIN 31 223	Tumor necrosis factor receptor
TRANSMEM 224 244	superfamily member 3.
REPEAT DOMAIN 245 415	Extracellular (Potential).
REPEAT 42 81	Cytoplasmic (Potential).
REPEAT 82 124	TNFR-Cys 1.
REPEAT 125 170	TNFR-Cys 2.
REPEAT 171 213	TNFR-Cys 3.
DISULFID 43 58	TNFR-Cys 4.
DISULFID 59 72	BY Similarity.
DISULFID 62 80	BY Similarity.
DISULFID 83 98	BY Similarity.
DISULFID 101 116	BY Similarity.
DISULFID 104 124	BY Similarity.
DISULFID 126 132	BY Similarity.
DISULFID 139 150	BY Similarity.
DISULFID 142 169	BY Similarity.
DISULFID 172 187	BY Similarity.
CARBORYD 40 40	N-Linked (GlcNAc. . .) (Potential).
CARBORYD 179 179	N-Linked (GlcNAc. . .) (Potential).
SEQUENCE 415 AA; 44956 MW;	29B32GA566AEFF661 CRC64;
Query Match 68.0%	Score 771; DB 1; Length 415;
Best Local Similarity 70.7%	Prd. No. 3.5e-57;
Matches 135; Conservative 14; Mismatches 40;	Indels 2; Gaps 1;
1 SOEQAVPPYASENQTCRDQKEYEPOHRICCSRCPPGTYSVAKCSRIRDTCATCAENS 60	
28 SQQLVPYRIEQTCWQDKEYEPMPHDVCCSSCPGPFFVAVCQRSDDTVCKTCPHNS 87	
61 YNEHHWNYLTICQLCRPCDPVMGLIEEIAPTSKRKTKQRCCQPGMFCAAVALETHC--ELL 118	

Db	88	YNEHWNHNLSTCQLCRPDIVLGEEVAPCTSDRKAECRCGPMSGCVLDNEVCHEERL	147
Qy	119	SDCPPGTBAELKDEVGKGNHNCVKPGKAGHFQNTSSPSPARCPQPHTRCENGVLVEAAGTAA	178
Db	148	VICQPETEEAFYDEIMTVDNVCVKPCFKOHFQNTSSPSPARCPQPHTRCENGVLVEAAGTAA	207
Qy	179	SDTICKNPPLP	189
Db	208	SDTICKNPPEP	218
RESULT 3			
Q800K7		PRELIMINARY;	PRT; 483 AA.
ID	Q800K7;		
AC	Q800K7;		
DT	01-JUN-2003	(TREMBLrel. 24, Created)	
DT	01-JUN-2003	(TREMBLrel. 24, Last sequence update)	
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)	
DR		Tumor necrosis factor receptor-2.	
GN		Name-TNFR-2;	
OS		Paralichthys olivaceus (Japanese flounder).	
OC		Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
OC		Actinopterygii; Neopterygii; Teleostei; Buteleosteoi; Neofishes;	
OC		Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;	
OC		Pleuronectoidei; Paralichthyidae; Paralichthys.	
RN	[1]	NCBI_TaxID=8255;	
RN		SEQUENCE FROM N.A.	
RP		REDFINE=22518447; PubMed=12631519; DOI=10.1016/S0145-305X(02)00118-0;	
RA		PARK C., Kurobe T., Hirose I., Aoki T.;	
RT		"Cloning and characterization of cDNAs for two distinct tumor necrosis factor receptor superfamily genes from Japanese flounder Paralichthys olivaceus";	
RT		Dev. Comp. Immunol. 27:365-375 (2003).	
RL		EMBL; AB00947; BAC5226.1; .	
DR	HSSP:	Q92356; JMA.	
DR	GO:	GO:0016021; C:integral to membrane; IEA.	
DR	GO:	GO:0004772; P:receptor activity; IEA.	
DR	GO:	GO:0005031; F:tumor necrosis factor receptor activity; IEA.	
DR	GO:	GO:0019221; P:cystokine and chemokine mediated signaling P. . ; IEA.	
DR	InterPro:	IPR013667; TNFR_recept_2.	
DR	InterPro:	IPR013687; TNFR_c6_-.	
DR	Pfam:	PF00020; TNFR_C6_-.	
DR	PIRS:	PIRS001968; TNFR_2; .	
DR	SMART:	SM00208; TNFR_4.	
DR	PROSITE:	PS00652; TNFR_NGFR_1; UNKNOWN_1.	
DR	PROSITE:	PS00500; TNFR_NGFR_2; .	
KW	Receptor.		
SEQUENCE	483 AA;	52227 MW; EEB55074A8C7F2085 CRC64;	
Query Match	27.3%	Score 309.5; DB 2; Length 483;	
Best Local Similarity	35.4%	Pred. No. 4. 3e-18;	
Matches	64;	Conservative 20; Mismatches 80; Indels 17; Gaps 6;	
Qy	16	CRDQEKEYEFOHRICCSRCPPGTYVSAKCSRIRDTCATCAENSYNEHWNLYTICQLCR	75
Db	27	CHNSTTVEYEQD--LCCKKCQPGQRLIQKCSQDATESVQKCDSQYMEKRNYAQKCLSCN	84
Qy	76	PCDPYQGLBEAPCTSKRKTQCRCPGFCAAWALE----CTHCELLSDCPPTGBAELK	130
Db	85	KCKSNKGQYAQCRCSSTTRTGCVKPGMYC--IMDFDNPYCAECRNTSQCRAGYGVSLP	141
Qy	131	DBVGKNNN--HCVPCKAGHFQNTSSPSPARCPQPHTRCENGVLVEAAGTAAQSDDTCKNPLE	188
Db	142	--GRANSIDVRCFLCPGMFSNTSNNETCRPHTDCIGKAVVR-KGNTFTSDTVCEEGVA	196
Qy	189	P 189	
Db	197	P 197	

- TR1B\_HUMAN STANDARD; PRT; 461 AA.  
 ID TR1B\_HUMAN STANDARD; PRT; 461 AA.  
 AC P61042; Q61129; Q9UHZ1;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 28-JAN-2003 (Rel. 41, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor 2) (TNF-R2) (Tumor necrosis factor receptor type II) (p75) (p80 TNF-alpha receptor) (CD120b) (Franneret)  
 DB [Contains: Tumor necrosis factor binding protein 2 (TNFR2-2)].  
 GN Name="TNFRSF1B"; Synonyms="TNFRF, TNFR2;"  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=9066639; PubMed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dower S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of  
 cellular and viral proteins.";  
 RT Science 248:1019-1023(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-196.  
 RX MEDLINE=9045991; PubMed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.B., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 naturally occurring tumor necrosis factor inhibitor.";  
 RP Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=96298745; PubMed=861109; DOI=10.1006/geno.1996.0327;  
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jansen S.J.,  
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desnauve F.J.,  
 RA Brodeur G.M.;  
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RN Genomics 35:94-100(1996).  
 RP SEQUENCE FROM N.A. (ISOFORM 2), SUBCELLULAR LOCATION, AND FUNCTION OF  
 RX ISOFORM 2.  
 RA PubMed=14688072; DOI=10.1033/intimm/dhx014;  
 RA Picart W., Engel P., Fernández-Real J.M., Romero X., Esplugues E., Canete J.D.,  
 RT "Identification and characterization of a novel spliced variant that  
 encodes human soluble tumor necrosis factor receptor 2.";  
 RI Int. Immunol. 16:169-177(2004).  
 RN [5]  
 RP SEQUENCE FROM N.A., AND VARIANTS MET-187; ARG-196; LYS-232; THR-236;  
 RP PRO-264 AND ARG-295.  
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W., Poel C.L., Robertson P.D.,  
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
 RA Schackwitz W.S., Sherwood J.K., Wittek L.A., Nickerson D.A.;  
 RT "NIEHS-SNPs, environmental genome project, NIEHS ES15479, Department  
 of Genome Sciences, Seattle, WA (URL: http://egg.gs.washington.edu)." ;  
 RT Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND  
 RP ARG-301.  
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,  
 RA Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,  
 RA Nickerson D.A.;  
 RT "SeattleSNPs: NHGRI HG66682 program for genomic applications," UW-  
 RT FHRC, Seattle, WA (URL: http://pga.gs.washington.edu);  
 RI Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=ENS.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Krausser R.L., Feingold B.A., Grouse L.H., Derge J.G., Goeddel D.V.;  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.P., Bhat N.K.,  
 RA Hsieh F., Max S.I., Wang J., Hong L., Rubin G.M., Farmer A.A.,  
 RA Diatchenko L., Marusina K., Brownstein M.F., Casper T.L., Schatz T.E.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Toshiyuki S., Carninci P., Prange C.,  
 RA Brownstein M.J., Usdin T.B., Loquellano N.A., Peters G.J., Abramson R.D., Mulahy S.J.,  
 RA Rah S.S., Richards S., McEvany P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting M.J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwade J., Schmidt J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schein A., Schein J.E., Jones S.J.M., Marras M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [8]  
 RP SEQUENCE OF 37-461 FROM N.A. (ISOFORM 1).  
 RX MEDLINE=91370690; PubMed=1966549; DOI=10.1016/1043-4666(90)90022-L.  
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,  
 RA Brockhaus M., Lesslauer W.;  
 RT "Two human TNF receptors have similar extracellular, but distinct  
 RT intracellular, domain sequences.";  
 RL Cytokine 2:231-237(1990).  
 RN [9]  
 RP SEQUENCE OF 116-461 FROM N.A. (ISOFORM 1), PARTIAL SEQUENCE, AND  
 RP VARIANT ARG-196.  
 RX MEDLINE=90349572; PubMed=2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
 RA Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor and  
 RT demonstration of a shed form of the receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155 (1990).  
 RN [10]  
 RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.  
 RX MEDLINE=21069356; PubMed=11197692; DOI=10.1038/sj.gene.6363700;  
 RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;  
 RT "New single nucleotide polymorphisms in the coding region of human  
 RT TNFR2: association with systemic lupus erythematosus.";  
 RL Genes Immun. 1:501-503 (2000).  
 RN [11]  
 RP SEQUENCE OF 27-31.  
 RC TISSUE=Urine;  
 RX MEDLINE=90110215; PubMed=2153136;  
 RA Engleman H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human urine.  
 RT Evidence for immunological cross-reactivity with cell surface tumor  
 RT necrosis factor receptors.";  
 RL J. Biol. Chem. 265:1531-1536 (1990).  
 RN [12]  
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE=91056048; PubMed=2173696;  
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two distinct  
 RT tumor necrosis factor receptors from HL60 cells.";  
 RL J. Biol. Chem. 265:20131-20138 (1990).  
 RN [13]  
 RP CHARACTERIZATION.  
 RX MEDLINE=93016104; PubMed=1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor  
 RT phosphorylation.";  
 RL J. Biol. Chem. 267:21172-21178 (1992).  
 RN [14]  
 RP INTERACTION WITH TRAF2.  
 RX MEDLINE=94349371; PubMed=8069116; DOI=10.1016/0092-8674(94)90532-0;  
 RA Rothe M., Wong S.C., Henzel D.V.;  
 RT "A novel family of putative signal transducers associated with the  
 RT cytoplasmic domain of the 75 kDa tumor necrosis Factor receptor.";



"Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific."; Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).  
 [2] RX SEQUENCE FROM N.A.  
 MEDLINE=11245168; PubMed=1645445;  
 RA Goodwin R.G.; Anderson D.J.; Jerzy R.; Davis T.; Brannan C.I.,  
 Copeland N.G.; Jenkins N.A.; Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 receptors for tumor necrosis factor.";  
 Mol. Cell. Biol. 11:3020-3026 (1991).  
 [3] RN  
 RP SEQUENCE FROM N.A.  
 MEDLINE=98414512; PubMed=9740674; DOI=10.1006/geno.1998.5407;  
 RA Hurle B.; Segade F.; Rodriguez R.; Ramos S.S.; Lazo P.S.;  
 RT "The mouse tumor necrosis factor receptor 2 gene: genomic structure  
 and characterization of the two transcripts.";  
 Genomics 52:79-98 (1998).  
 [4] RN  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RC STRAIN=NOD;  
 RA Jacob C.O.; Liu J.J.;  
 RI Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.  
 [5] RN  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=Liver;  
 RA Kisseljovska M.; Fellowes R.; Feldmann M.; Chernajovsky Y.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.  
 CC -1- FUNCTION: Receptor with high affinity for TNFRSF2/TNF-alpha and  
 approximately 5-fold lower affinity for homotrimeric  
 TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the  
 apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By  
 similarity).  
 CC -1- SUBUNIT: Binds to TRAF2 (By similarity).  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
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 or send an email to license@isb-sib.ch).  
 CC  
 DR AA39752; 1; -.  
 DR EMBL; M59378; AA40463; 1; -.  
 DR EMBL; Y14619; CAFA74969; 1; -.  
 DR EMBL; Y14620; CAFA74969; 1; JOINED.  
 DR EMBL; Y14621; CAFA74969; 1; JOINED.  
 DR EMBL; Y14622; CAFA74969; 1; JOINED.  
 DR EMBL; Y14679; CAFA74969; 1; JOINED.  
 DR EMBL; Y14623; CAFA74969; 1; JOINED.  
 DR EMBL; U39488; AA485021; 1; -.  
 DR EMBL; X87128; CAFA6018; 1; -.  
 DR PIR; B38634; B38634.  
 DR HSSP; B19436; INCFP.  
 DR MED; MG1:1314883; Tnfrsf1b; IMP.  
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . ; IMP.  
 DR GO; GO:0006554; P:inflammatory response; IMP.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PIRSF; PIRSP001958; TNFR\_2; 1.  
 DR SMART; SM00208; TNFR\_4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 SIGNAL 1 22  
 FT CHAIN 23 474 Tumor necrosis factor receptor superfamily member 1B.  
 FT DOMAIN 23 258 Extracellular (Potential).

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PT TRANSMEM 259 288 Potential: Cytoplasmic (Potential).  
 PT DOMAIN 289 474 TNFR-Cys 1.  
 PT REPEAT 339 77 TNFR-Cys 2.  
 PT REPEAT 78 119 TNFR-Cys 3.  
 PT REPEAT 120 164 TNFR-Cys 4.  
 PT DISULFID 165 203 TNFR-Cys 5.  
 PT DISULFID 40 54 By similarity.  
 PT DISULFID 55 68 By similarity.  
 PT DISULFID 58 76 By similarity.  
 PT DISULFID 79 94 By similarity.  
 PT DISULFID 97 111 By similarity.  
 PT DISULFID 101 119 By similarity.  
 PT DISULFID 121 127 By similarity.  
 PT DISULFID 136 145 By similarity.  
 PT DISULFID 139 163 By similarity.  
 PT DISULFID 166 181 By similarity.  
 PT CARBOHYD 69 69 N-linked (GlcNAc. . ) (Potential).  
 PT CARBOHYD 195 195 N-linked (GlcNAc. . ) (Potential).  
 PT CONFLICT 78 78 D-> DSDIVCAG (in Ref. 3).  
 PT CONFLICT 102 102 T-> S (in Ref. 3).  
 PT CONFLICT 108 108 T (in Ref. 3).  
 PT CONFLICT 283 283 I-> F (in Ref. 3).  
 PT CONFLICT 331 331 S-> SS (in Ref. 3).  
 PT CONFLICT 360 360 F (in Ref. 3).  
 PT CONFLICT 436 436 C-> Y (in Ref. 3).  
 SQ SEQUENCE 474 AA; 50319 MW; 462EA398C4D553 CRC64; Query Match 26.0%; Score 295; DB 1; Length 474;  
 CC Best Local Similarity 34.0%; Pred. No. 7 1e-17;  
 Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;

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Qy 8 PYASE-NOTCRDQEKEYEYEPQRICCSRCPRTGTYSAKCSRIRDTCATCAENSYNEHWN 66  
 Db 31 PYKPEPEYECOISQ-PXYDRAQMCCAKCPQQYURHFMCNKTSDTVCADCEASMTQWN 89  
 Qy 67 YLTICQLCR--PCDPVNGLEBIAPTTSKTKTQRQCOPGMCA--AWALBCTHCELLSDC 121  
 Db 90 QFRTCLSCSSSCTTDQV---EIRACTKQONRVACEAGRYCALTHSGSCRQKRLSKC 145  
 Qy 122 PPGTAEBLKDEVKGNNHCVPCKA GHFQNTSSPSARCOPHTRCENGQGLVEAAPGTAQSDT 181  
 Db 146 GPGP-GYASSRAPNGVNLCKACAPTFSDTSSTDVCRPHICS---ILAIPGNASTDA 200  
 Qy 182 TCKNPYLEPLPPEMS 195  
 Db 201 VC---APESPTLS 210  
 RESULT 7 Q91ZM6 PRELIMINARY; PRT; 433 AA.  
 ID Q91ZM6 AC Q91ZM6 PRELIMINARY; PRT; 433 AA.  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Tumor necrosis factor receptor type II (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1] NCBI\_TaxID=10116;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=22263089; PubMed=12376316;  
 RA Osberg B.; Peiser C.; Domling D.; Schomburg L.; Ko Y.T.; Voigt K.;  
 RA Bickel U.;  
 RT "Effect of endotoxin on expression of TNF receptors and transport of  
 TNF-alpha at the blood-brain barrier of the rat";  
 RL Am. J. Physiol. Endocrinol. Metab. 283:E899-E908(2002).  
 DR EMBL; AF420214; AAI6021; -.  
 DR HSSP; P19338; INCFC.  
 DR GO; GO:0004872; F:receptor activity; IER.  
 DR Pfam; PF00020; TNFR\_C6; 2.

DR SMART; SM00208; TNFR; 4.	Db 85 LHTCLCSSSCSDDQV---ETHNCTKQNRCVACNAKDSYCALKHLHSGNCRQCMKLSKCG 140
DR PROSITE; PS00652; TNFR_NGFR_1; 2.	Qy 123 PGTEABLRDEVGKNNHCVPKRAGHFTNTSSPARCPHTRGENGLVEAAGPTAQSDTT 182
DR PROSITE; PS50050; TNFR_NGFR_2; 3.	Db 141 PGF-GVARSRTSGNGNVICSAACPTFSDTTSSTDVCRPHRICs---ILAFGNASTDAV 195
KW Receptor.	Qy 183 CRNPFLPPLPEMSGT 197
FT NON_TER 1 1	Db 196 CASE-SPPSAVRT 209
SQ SEQUENCE 433 AA; 433 MW; 75736D835E72CA4A CRC64;	
Query Match 8 PYASENQTCRDQEKEYBPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENSYNEHWY 67	RESULT 9
Best Local Similarity 33.3%; Pred. No. 1.3e-16; Length 433;	TRIB_RAT ID TRB_RAT STANDARD; PRT; 474 AA.
Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;	AC Q80WY6; DT 25-JAN-2005 (Rel. 46, Created)
Db 11 PYKEPBGHQCQISQEYTKRAQNCACKPGQAKHFRNKTSDTVCADCAAGMFTQWNH 70	DT 25-JAN-2005 (Rel. 46, Last sequence update)
Qy 68 LITCQLC-RPC--DPVNGLIEETAPCTSRRKTKTQCRCPGMFCA - AWALECTCELLSDCP 122	DT 25-JAN-2005 (Rel. 46, Last annotation update)
Db 71 LHPTLCSSSCSQSDQV---ETHNCTKQNRCVACNAKDSYCALKHLHSGNCRQCMKLSKCG 126	DE Tumor necrosis factor receptor superfamily member 1B precursor ("tumor necrosis factor receptor type 2") (TNF-R2) ("Tumor necrosis factor receptor type II") (p75) (p80 TNF-alpha receptor).
Qy 123 PGTEABLRDEVGKNNHCVPKRAGHFTNTSSPARCPHTRGENGLVEAAGPTAQSDTT 182	DE Name=tnfrsfib; Synonyms=tnfr2;
Db 127 PGF-GVARSRTSGNGNVICSAACPTFSDTTSSTDVCRPHRICs---ILAFGNASTDAV 181	GN Ratius norvegicus (Rat).
Qy 183 CRNPFLPPLPEMSGT 197	OS Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Db 182 CASE-SPPSAVRT 195	OX NCBI_TaxID=10116;
RN [1]	RN RN
RESEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC STRAIN=Wiistar; TISSUE=Spleen;	RC RA Li Y.; Ji A.; Schafer M.K.;
RA "Expression of TNFR2 in rat dorsal root ganglion".	RA RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL "Expression of TNFR2 in rat dorsal root ganglion".	RL CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and approximately 5-fold lower affinity for homotrimeric TNFSF1/Lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By similarity).
CC -1- SUBUNIT: Binds to TRAF2 (By similarity).	CC CC
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).	CC CC
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.	CC CC
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CC	CC
RESULT 8 Q6VAU8 PRELIMINARY; PRT; 461 AA.	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
ID Q6VAU8; AC DR 05-JUL-2004 (TrEMBLrel. 27, Created)	CC DR HSSP; P19438; INCf.
DR 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	DR RGD; 621238; Trnrsf1b.
DR 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	DR InterPro; IPR001368; TNFR_c6.
DR Tumor necrosis factor receptor type 2 (Fragment).	DR InterPro; IPR011366; TNFrRecept_2.
OS Rattus norvegicus (Rat).	DR Pfam; PF00020; TNFR_C6; 2.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	DR PIRSP; PISSP001968; TNFR_2; 1.
OX NCBI_TaxID=10116;	DR SMART; SM00208; TNFR_2; 1.
RN RN	DR PROSITE; PS00652; TNFR_NGFR_1; 2.
RESEQUENCE FROM N.A.	DR PROSITE; PS50050; TNFR_NGFR_2; 3.
RC STRAIN=Wiistar; TISSUE=Spleen;	KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
RA Inglis J.J.; Chernajovsky Y.; Kidd B.L.;	FT SIGNAL 1 22 By similarity.
DR Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.	FT CHAIN 23 474 Tumor necrosis factor receptor superfamily member 1B; Extracellular (Potential).
DR Y344841; AAQ22350.1; -	FT DOMAIN 23 258 Potential.
DR GO; GO:0016021; C:integral to membrane; IEA.	FT TRANSMEM 259 288 Cytoplasmic (Potential).
DR GO; GO:004812; F:receptor activity; IEA.	FT DOMAIN 289 474
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IEA.	FT REPEAT 39 77 TNFR-Cys 1.
DR GO; GO:019221; P:cytokine and chemokine mediated signaling p. . . IEA.	FT REPEAT 119 119 TNFR-Cys 2.
DR InterPro; IPR011366; TNFrRecept_2.	FT REPEAT 120 164 TNFR-Cys 3.
DR InterPro; IPR001368; TNFR_c6.	FT DISULFID 165 203 By similarity.
DR Pfam; PF00020; TNFR_c6; 2.	FT DISULFID 40 54 By similarity.
DR PIRSP001968; TNFR_2; 1.	FT DISULFID 55 68 By similarity.
DR SMART; SM00208; TNFR_4.	FT DISULFID 58 76 By similarity.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.	
KW Receptor.	
FT NON_TER 1 1	
SQ SEQUENCE 461 AA; 461 MW; B36769C080B1308A CRC64;	
Query Match 8 PYASENQTCRDQEKEYBPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENSYNEHWY 67	
Best Local Similarity 33.3%; Pred. No. 1.4e-16; Length 461;	
Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;	
Db 25 PYKEPBGHQCQISQEYTKRAQNCACKPGQAKHFRNKTSDTVCADCAAGMFTQWNH 84	
Qy 68 LITCQLC-RPC--DPVNGLIEETAPCTSRRKTKTQCRCPGMFCA - AWALECTCELLSDCP 122	

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FT	DISULFID	97	111	By similarity.	DR PROSITE; PS00652; TNFR_NGFR_1; 2.
FT	DISULFID	101	119	By similarity.	DR PROSITE; PS50050; TNFR_NGFR_2; 3.
FT	DISULFID	121	127	By similarity.	KW Receptor.
FT	DISULFID	136	145	By similarity.	FT NON_TER
FT	DISULFID	139	163	By similarity.	FT NON_TER
FT	DISULFID	166	181	By similarity.	SQ SEQUENCE
FT	CARBOND	69	69	N-linked (GICNAC. . .) (Potential).	459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;
FT	CARBOND	110	110	N-linked (GICNAC. . .) (Potential).	Query Match 25.6%; Score 290; DB 2; Length 459;
FT	CARBOND	195	195	N-linked (GICNAC. . .) (Potential).	Best Local Similarity 33.5%; Pred. No. 1.8e-16;
SQ	SEQUENCE	474 AA;	50148 MW;	298C6AB9E8C8D714 CRC64;	Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;
Query Match		25.7%	Score 291.5;	Pred. No. 1.4e-16;	Query 8 PYASE-NOTCRDQEKEYYEPORHICCSRQPPTGTVSAKCSRIRDTCATCAENSYNEHWW 66
Best Local Similarity	33.3%	Pred. No. 1.4e-16;	DB 1;	Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;	Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;
Matches	65;	Conservative	24;	Pykpepyecqiso-Eyydrkaqmcakcpqgoytkhfcnktstvcadceasmytqvwn 74	Pykpepyecqiso-Eyydrkaqmcakcpqgoytkhfcnktstvcadceasmytqvwn 74
Qy		8	PYASE-NOTCRDQEKEYYEPORHICCSRQPPTGTVSAKCSRIRDTCATCAENSYNEHWW 67	Db 16 PYKPEPYECQISO-EYYDRKAQMCACKCPQGQYTKHFCNKTSTVCADCEASMYTQVWN 74	
Db		31	Pykpepyecqiso-qeyyeporhiccsrqppgtysakcsrirdtcataensynewww 67	Qy 67 YLTICOLCR --PCDFVMGLEEIAPTCSKRKTKOCTCQPGMFCA - -AWALEBCTHCBLSDC 121	
Qy		68	LTCQLC-LRPC --DPVNGCLEEIAPTCSKRKTKOCTCQPGMFCA - -AWALEBCPHCELLDCP 122	Db 75 QFRTLUSCSSSCSTDQV --ETRACTKQONRVCAEAGYCALTHSGCRQMLSLSK 130	
Db		91	LHTCLSSSSCSQSDQV --ETHNCTKKQNRYCAACNAADSVCALKLHSQNCRQCMKLISKCG 146	Qy 122 PPGTEAELKDVEKGKGNHCUPCKAGH FRONTISSPSARCOPHTRCENOGLVAAAPGTAOQSDTT 181	
Qy		123	PGTEAELKDVEKGKGNHCUPCKAGH FRONTISSPSARCOPHTRCENOGLVAAAPGTAOQSDTT 182	Db 131 GPPGF-GVASSRAPNGVNLCKACAPGTESDTTSSTIVCRPHRICSS---IIAIPGNASTDA 185	
Db		147	GPGF-GVASSRPTSGNVLTCACAPGTFSITTSSTIVCRPHRICSS---IIAIPGNASTDAV 201	Qy 182 TCKNPPLPPLPEMS 195	
Qy		163	CKNPPLPPLPEMSGT 197	Db 186 VC--APBSPTLS 195	
Db		202	CASE-SPTPSAVRT 215		
RESULT 11					
TR6B_HUMAN	ID	TR6B_HUMAN	STANDARD;	PRT;	300 AA.
AC	ID	095407;			
AC	ID	095407;	Rel. 41, Created)	DT 28-FEB-2003 (Rel. 41, Last sequence update)	
AC	ID	095407;	Rel. 41, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last sequence update)	
DB	ID	05-TUI-2004 (Rel. 44, Last annotation update)		DT 05-TUI-2004 (Rel. 44, Last annotation update)	
DB	ID	DB receptor for Fas ligand) (Decoy receptor 3) (DCR3) (Ms8)		DB receptor for Fas ligand) (Decoy receptor 3) (DCR3) (Ms8)	
DE	ID	(UNQ186/PRO212).			
GN	ID	Name=INFR6B;			
OS	ID	Homosapiens (Human).			
OC	ID	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	ID	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	ID	NCBI_Taxid=9606;			
RN	ID	[1]			
RP	ID	SEQUENCE FROM N.A.			
RC	ID	TISSUE=Fetal lung;			
RX	ID	MEDLINE=92087326; PubMed=987321; DOI=10.1038/25387;			
RA	ID	Pitti R.M., Marsters S.A., Lawrence C.J., Kischkel F.C.,			
RA	ID	Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,			
RA	ID	Godowski P.J., Wood W.I., Gurney A.L., Hillian K.J., Cohen R.L.,			
RA	ID	Goddard A.D., Botstein D., Ashkenazi A.,			
RA	ID	"Genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer";			
RL	ID	J. Biol. Chem. 274:13733-13736(1999).			
RN	ID	[2]			
RP	ID	SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.			
RC	ID	TISSUE=Prostate;			
RX	ID	MEDLINE=99053915; PubMed=10318773; DOI=10.1074/jbc.274.20.13733;			
RA	ID	Powell B.E., Wicker L.S., Peterson L.B., Todd J.A.;			
RT	ID	"Allelic variation of the type 2 tumor necrosis factor receptor gene."			
RT	ID	Mamm. Genome 5:76-77(1994).			
RL	ID	DR EMBL; X76401; CA53981.1; -.			
DR	ID	DR HSSP; E19854; I48954.			
DR	ID	DR HSSP; E19438; INPF.			
DR	ID	DR SGD; MG1:131483; Tnfrcslb.			
DR	ID	DR GO:0005615; C:extracellular space; TAS.			
DR	ID	DR GO:0016021; C:integral to membrane; TAS.			
DR	ID	DR GO:0008283; B:cell proliferation; TAS.			
DR	ID	DR GO:0007166; P:cell surface receptor linked signal transdu... ; IMP.			
DR	ID	DR GO:0006554; B:inflammatory response; IMP.			
DR	ID	DR InterPro; IPR001368; TNFR_C6; 2.			
DR	ID	DR Pfam; PF00020; TNFR_C6; 2.			





PT	DISULPID	51	69	By similarity.	Db	22	PPTA-----CR-EKQYLINSO--CCSLCQEQKLVSDCDTEPCGSEFDTWN 72
PT	DISULPID	72	87	By similarity.	QY	67	YLTICOLCRPCDPVMLEIACTSRKTKQRCPGMFCAAWALECTCELLSDCPOTE 126
PT	DISULPID	93	113	By similarity.	Db	73	RETHQOHKYCUPNLGLRVQOKTSETDTCTICEGWHCTSEA-CESCVLHRSSCPFG 130
PT	DISULPID	115	128	By similarity.	QY	127	ABRKEDEVKGNNHCVPCKAGHQNTSSPSARCQPHRCENQSLVEAAGTAQSDDTC 183
PT	CARBOHYD	134	152	N-linked (GlcNAc. . .) (Potential).	Db	131	VK-QIATGVSDTICECPVGPFSNVSSAPEKCHPWTSCETDLVQQAGTNKTVDVC 186
PT	CARBOHYD	106	106	N-linked (GlcNAc. . .) (Potential).	QY	131	VK-QIATGVSDTICECPVGPFSNVSSAPEKCHPWTSCETDLVQQAGTNKTVDVC 186
PT	CARBOHYD	175	175	N-linked (GlcNAc. . .) (Potential).	QY	131	VK-QIATGVSDTICECPVGPFSNVSSAPEKCHPWTSCETDLVQQAGTNKTVDVC 186
PT	CONFLICT	494	494	R -> K in Ref. 21.	DB	131	VK-QIATGVSDTICECPVGPFSNVSSAPEKCHPWTSCETDLVQQAGTNKTVDVC 186
SQ	SEQUENCE	625	AA:	66621 MW;	DB	131	VK-QIATGVSDTICECPVGPFSNVSSAPEKCHPWTSCETDLVQQAGTNKTVDVC 186
Query Match		25.0%	Score 283;	DB 1;	Length 625;	RESULT 15	
Best Local Similarity		32.6%	Pred. No. 9.	g-e-16;		TNRS_HUMAN	STANDARD;
Matches		60;	Conservative	25;	Mismatches 85;	ID TNRS_HUMAN	PRT: 277 AA.
QY		4	QAVPPYASENOTCRDQEKEYEPOHRICCSRCPPGTYYSAKCSRIRDTCATCAENSYE 63			AC P25942; Q9BYU0;	
DB		30	QVTTPCCTOE-----RHYEHLGR-CCSRCEBGPYTLISKCTPDSVCLPGPDEVLY 79			DT 01-MAY-1992 (Rel. 22, Created)	
QY		64	HNNYLITICOLCRPCDPVMLEIACTSRKTKQRCPGMFCAAWALECTCELLSDOPP 123			DT 01-MAY-1992 (Rel. 22, Last sequence update)	
DB		80	TWNBEDBKULHKVCDAGKALVADPGNNTAPRERACTAGYH--WNSNCSECCRNTTCAP 136			DT 25-JAN-2005 (Rel. 46, Last annotation update)	
QY		124	GTERABLKEDEVKGNNHCVPCKAGHQNTSSPSARCQPHRCENQLYVEAAGTAQSDDTC 183			DB Tumor necrosis factor receptor superfamily member 5 precursor (CD40L)	
DB		137	GFGAQHPLQLNK-DTVCTPCLLGFFSDVFSSTDKCKPWTNCNTLGLKLEAHQGTTESDVVC 195			DE receptor (B-cell surface antigen CD40) (CDW40) (Bp50).	
QY		184	KNPL 187			GN Name=TNFRSF5; Synonyms=CD40;	
DB		196	SSSM 199			OS Homo sapiens (Human); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
QY		25	;			OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
DB		25	;			NCBI_TaxID=9606;	
Q867KS		PRELIMINARY;	PRT;	223 AA.		RN [1]	
AC		Q867KS;	PRT;	223 AA.		RN [2]	
DT	01-JUN-2003	(TREMBLrel. 24, Created)				RP SEQUENCE FROM N.A. (ISOFORM II).	
DT	01-JUN-2003	(TREMBLrel. 24, Last sequence update)				RX MEDLINE=21117110; PubMed=1172223; DOI=10.1073/pnas.98.4.1751;	
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)				RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;	
DB		Tumor necrosis factor receptor superfamily member 5 (Fragment).				RA "Regulation of CD40 function by its isoforms generated through RT alternative splicing";	
GN		Name=TNFRSF5;				BL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756 (2001).	
OS		Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				RN [3]	
OC		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				RP SEQUENCE FROM N.A. (ISOFORM I), AND VARIANT S LBU-124 AND ALA-227.	
OX		NCBI_TaxID=9606;				RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood A.M., Leithauer B.J., Nickerson D.A.;	
RN						RA RT "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp-98.washington.edu).";	
RP		SEQUENCE FROM N.A.				RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.	
RA		He X., Xu L., Zeng Y.; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				RN [4]	
DR		EMBL: AV225405; AAC043950.1; -.				RP SEQUENCE FROM N.A.	
DR		HSSP; Q92956; 1UTM.				RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;	
DR		GO: GO:00016020; C:membrane; IEA.				RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Jones M., Stavridis G., Almeida J.P., Babbuley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burkill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Cleo C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graffham D.V., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Hucke B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehaeslainio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovall J.D., Marsh V.L., Martin S., McConnaichie L.J., McInlay K., McMurray A.A., Milne S.A., Misra D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Philimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Sims S., Skuse C.M., Ross M.T., Scott C.E., Sehra H.K., Showmen R., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Trromans A.C., Vaudin M., Wall M., Wallis J.M.,	
Query Match		24.5%	Score 278;	DB 2;	Length 223;		
Best Local Similarity		35.0%	Pred. No. 9.	g-e-16;			
Matches		20;	Mismatches 83;	Indels 12;	Gaps 5;		
QY		7	PPVASENQTCRDQEKEYEPOHRICCSRCPPGTYYSAKCSRIRDTCATCAENSYNHWN 66				

- RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wliming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.; "The DNA sequence and comparative analysis of human chromosome 20."; *Nature* 414:865-871(2001). [5]
- RP SEQUENCE FROM N.A. (ISOFORM I).
- RC TISSUE=Ovary;
- RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
- RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner U., Shenker C.M., Schaeffer C.P., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haileh F., Diatchenko L., Matsushita K., Farmer A.A., Rubin G.M., Hong L., Stoepler M., Soares M.B., Donald M.F., Casavant T.J., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C., Loquai-Lalio N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B., Kettemann M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Schmutz J., Dickson M.C., Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E., Scheiner A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903 (2002). [6]
- RN SEQUENCE OF 21-30.
- RX PMID=1167606; DOI=10.1006/prep.2001.1501;
- RA Khandekar S.S., Silverman C., Wells-Marear J., Bacon A.M., Birrell H., Brigham-Burke M., DeMarini D.J., Jonak Z.I., Camilleri P., Fishman-Lobell J.; "Determination of carbohydrate structures N-linked to soluble CD154 and characterization of the interactions of CD40 with CD154 expressed in Pichia pastoris and Chinese hamster ovary cells."; *Protein Expr. Purif.* 23:301-310(2001). [7]
- RX PMID=15340161; DOI=10.1110/ps.04682504;
- RA Zhang Z., Henzel W.J.; "Signal peptide prediction based on analysis of experimentally verified cleavage sites."; *Protein Sci.* 13:2819-2824 (2004).
- RN INTERACTION WITH TRAF3.
- RX MEDLINE=95184010; PubMed=7533327;
- RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D., RT "Involvement of Craf1, a relative of Traf1, in CD40 signaling."; *Science* 267:1494-1498 (1995). [8]
- RN INTERACTION WITH TRAF3.
- RX MEDLINE=95129692; PubMed=7530216; DOI=10.1016/0014-5793(94)01406-Q;
- RA Sato T., Irie S., Reed J.C., "A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40."; *J. Biol. Chem.* 271:301-310(2001). [9]
- RN INTERACTIONS WITH TRAF1; TRAF2; TRAF5;
- RX MEDLINE=98384149; PubMed=9718306; DOI=10.1021/bi981067q;
- RA Pullen S.S., Miller H.G., Everdean D.S., Dang T.T., Crute J.J., Kehry M.R.; "CD40-tumor necrosis factor receptor-associated factor (TRAF) interactions: regulation of CD40 signaling through multiple TRAF binding sites and TRAF hetero-Oligomerization."; *Biochemistry* 37:11836-11845 (1998). [10]
- RN INTERACTION WITH TRAF5;
- RX MEDLINE=98122745; PubMed=9511754; DOI=10.1016/S0378-1119(97)00616-1;
- RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M., Otsuka M., Yamamoto T., Inoue J.-I., "Tissue specificity of B-cells and primary carcinomas. Defects in TNFRSFs are the cause of hyper-IgM immunodeficiency type 3 (HIGM3) [MIM:60643]. HIGM3 is an immunodeficiency with hyper-IgM syndrome."; *Proc. Natl. Acad. Sci. U.S.A.* 98:12614-12619 (2001). [11]
- RN INTERACTION WITH TRAF5;
- RX MEDLINE=98122745; PubMed=9511754; DOI=10.1016/S0378-1119(97)00616-1;
- RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M., Otsuka M., Yamamoto T., Inoue J.-I., "Tissue specificity of B-cells and primary carcinomas. Defects in TNFRSFs are the cause of hyper-IgM immunodeficiency type 3 (HIGM3) [MIM:60643]. HIGM3 is an immunodeficiency with hyper-IgM syndrome."; *Proc. Natl. Acad. Sci. U.S.A.* 98:12614-12619 (2001). [12]
- RN INTERACTION WITH TRAF6.
- RX MEDLINE=98095703; PubMed=9432981;
- RA Kashiwada M., Shirakawa Y., Inoue J.-I., Nakano H., Okazaki K., Okumura K., Yanamoto T., Nagakura H., Take mori T.; "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates extracellular signal-regulated kinase (ERK) activity in CD40 signaling along a ras-independent pathway."; *J. Exp. Med.* 187:237-244 (1998). [13]
- RN 3D-STRUCTURE MODELING OF 247-144.
- RX MEDLINE=97189482; PubMed=9037712;
- RA DOI=10.1002/(SICI)1097-0134(19970127)27:1<59::AID-PROT7>3.0.CO;2-Z;
- RA Bajrachary J., Aruffo A.; "Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40."; *Proteins* 27:59-70 (1997). [14]
- RN 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
- RX MEDLINE=98266353; PubMed=1605317;
- RA Singh J., Garber E., van Vlijmen H., Karpuswas M., Hsu Y.-M., Zheng Z., Naismith J.H., Thomas D.; "The role of polar interactions in the molecular recognition of CD40L with its receptor CD40."; *Protein Sci.* 7:1124-1135 (1998). [15]
- RN X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH TRAF3.
- RX MEDLINE=20442386; PubMed=10984535; DOI=10.1073/pnas.97.19.10395;
- RA Ni C.Z., Welsh K., Leo E., Chiu C.K., Wu H., Reed J.C., Ely K.R.; RT "Molecular basis for CD40 signaling mediated by TRAF3."; *Proc. Natl. Acad. Sci. U.S.A.* 97:10395-10399 (2000). [16]
- RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH TRAF3.
- RX MEDLINE=22000222; PubMed=12005438; DOI=10.1016/S0969-2126(02)00733-5;
- RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C., Satterthwaite A.C., Cheng G., Ely K.R.; RT "Downstream regulator TANK binds to the CD40 recognition site on TRAF3."; *Structure* 10:403-411 (2002). [17]
- RN VARIANT HIGM3 ARG-83.
- RX MEDLINE=21532985; PubMed=11675497; DOI=10.1073/pnas.221456898;
- RA Ferrari S., Giliani S., Insalaco A., Al-Ghonaium A., Soresina A.R., Loubser M., Avanini M.A., Marconi M., Badoato R., Uggazio A.G., Levy Y., Catalani N., Durandy A., "Tbakhri A., Notarangelo L.D., Plebani A.; "Mutations of CD40 gene cause an autosomal recessive form of immunodeficiency with hyper IgM."; *Proc. Natl. Acad. Sci. U.S.A.* 98:12614-12619 (2001). [18]
- CC -1- FUNCTION: Receptor For TNFRSF5/CD40L;
- CC -1- SUBUNIT: Interacts With TRAF1; TRAF5; TRAF3; TRAF5 And TRAF6.
- CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform I); secreted (isoform II).
- CC -1- ALTERNATIVE PRODUCTS:
- CC Comment=Additional isoforms seem to exist;
- CC Name=I; IsoId=P25942-1; Sequence=Displayed;
- CC Name=II;
- CC IsoId=P25942-2; Sequence=VSP\_006473;
- CC -1- TISSUE SPECIFICITY: B-cells and in primary carcinomas.
- CC -1- DISEASE: Defects in TNFRSFs are the cause of hyper-IgM immunodeficiency type 3 (HIGM3) [MIM:60643]. HIGM3 is an immunodeficiency with hyper-IgM syndrome."; *Proc. Natl. Acad. Sci. U.S.A.* 98:12614-12619 (2001). [19]
- Query Match 24 %; Score 278; DB 1; Length 277;
- Best Local Similarity 35 %; Pred. No. 1.2e-15;
- Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

Qy	7	PPVYSENENOTCRDQEKEYYEFQHRI	CCSRCPGTYVSAKCSRIRIDIVCATAENSNEHWN	66
Db	22	PPTA----CR--BQYLINSQ-	CCSLCOPGOKLVSDEFTTFCPLPGESDTPDTWN	72
Qy	67	YLTCOLCRCPDCPMLGLEIAPCTSKRTIQCRQGMFCDAWALECTHCELLSDCPPGTE	124	
Db	73	RETHIQHQXCDPNLGLR/YQKGTSSETDATICTCERGMHCTSEA	-CESCYLHRSCSPGFG	134
Qy	127	AELKDEVGKGNHHNCYCPKAGHFPONTISSPSARQCPTTRCENQGLYEAAPTAQSDDTC	183	
Db	131	VK-OJATGVSDFTICBPCPVGFSSVSSAFAFKCHPMTCSECFKDVYOOAGTNTKTVYC	186	

Search completed: September 23, 2005, 10:30:34  
Job time : 177 secs

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